09/856819
JC18 Rec'd PCT/PTO 24 MAY 2001

Attorney Docket No.: 5559.204-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

Box PCT
Commissioner for Patents
Washington, DC 20231

Sir:

This is a request for filing a patent application under 35 U.S.C. 371 of the international application identified below:

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/DK99/00664	**November 29, 1999**	**November 27, 1998**

APPLICANT(S)/INVENTOR(S)

Given Name (First and middle (if any))	Family Name or Surname	Residence (City and Either State or Foreign Country)
1. Kirsten	1. Bojsen	1. DK-2900 Hellerup, Denmark
2. Allan	2. Svendsen	2. DK-2970 Hørsholm, Denmark
3. Claus Crone	3. Fuglsang	3. DK-2990 Nivå, Denmark
4. Shamkant Anant	4. Patkar	4. DK-2800 Lyngby, Denmark
5. Kim	5. Borch	5. DK-3460 Birkerød, Denmark
6. Jesper	6. Vind	6. DK-2880 Lyngby, Denmark
7. Andreas	7. Petri	7. DK-2200 Copenhagen, Denmark
8. Sanne O. Schrøder	8. Glad	8. 2750 Ballerup, Denmark
9. Gitte	9. Budolfsen	9. DK-2000 Frederiksberg, Denmark

TITLE OF THE INVENTION

Lipolytic Enzyme Variants

1. This is a first submission of items concerning a filing under 35 U.S.C. 371
2. This is an express request to begin national examination procedures (35 U.S.C. 371(f)).
3. The US has been elected by the expiration of 19 months from the priority date (Article 31).
4. A copy of the International Application as filed (35 U.S.C. 371(c)(2)) has been communicated by the International Bureau on June 3, 2001.
5. An oath or declaration of the inventors is submitted herewith.
6. An Information Disclosure Statement is submitted herewith.
7. An Assignment and Recordation Form Cover Sheet are submitted herewith.

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8. A Preliminary Amendment is submitted herewith.

9. A computer-readable form of the sequence listing is submitted herewith.

10. The assignee of the present application is:

Novozymes A/S
Krogshoejvej 36
DK-2880 Bagsvaerd
Denmark

Applicants request that the assignee information be included in the published patent application.

11. Direct all correspondence to Customer Number 25908:

PATENT TRADEMARK OFFICE

25908

12. The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):

Search Report has been prepared by the EPO or JPO	$ 860
CLAIMS FEE	
Total Claims: 29 - 20 = 9 x 18 =	$ 162
Independent Claims: 3 - 3 = 0 x 80 =	$ 0
Total Claims Fee:	$ 162
FEE FOR RECORDING ASSIGNMENT	$ 40
TOTAL NATIONAL FEE	$ 1062

13. Please charge the required fee, estimated to be $1,062, to Novozymes North America, Inc., Deposit Account No. 50-1701. A duplicate of this sheet is enclosed.

Respectfully submitted,

Date: May 24, 2001

Jason I. Garbell, Reg. No. 44,116
Novozymes North America, Inc.
405 Lexington Avenue, Suite 6400
New York, NY 10174-6401
(212) 867-0123

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#7/B

Attorney Docket No.: 5559.204-US

PATENT

RECEIVED

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bojsen et al.

Confirmation No: To Be Assigned

Serial No.: 09/856,819

Group Art Unit: To Be Assigned

Filed: May 24, 2001

Examiner: To Be Assigned

For: Lipolytic Enzyme Variants

PRELIMINARY AMENDMENT

Box PCT
Commissioner for Patents
Washington, DC 20231

Sir:

Before examination, please amend the above-identified application as follows (a marked up version pursuant to 37 C.F.R. 1.21 is attached hereto):

IN THE SPECIFICATION:

At page 1, after the title, please replace the paragraph under the heading CROSS-REFERENCE TO RELATED APPLICATIONS, with the following paragraph:

.-- CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a 35 U.S.C. 371 national application of PCT/DK99/00664, filed November 29, 1999, and claims, under 35 U.S.C. 119, priority of Danish application nos. PA 1998 01572, filed November 27, 1998, PA 1999 00391, filed March 22, 1999, PA 1999 01481, filed October 15, 1999, the contents of which are fully incorporated herein by reference and the benefit under 35 U.S.C. 119(e) of United States provisional patent application nos. 60/111,430, filed on December 8, 1998, 60/126,914, filed on March 29, 1999, and 60/160,735, filed on October 22, 1999.--

REMARKS

This amendment is submitted to include in the CROSS-REFERENCE TO RELATED APPLICATIONS, Applicants claim to the benefit, under 35 U.S.C. 119(e), of United States provisional patent application nos. 60/111,430, 60/126,914 and 60/160,735. The claim to the benefit of these United States provisional applications was made in PCT/DK99/00664 and in the Combined Declaration For Utility Patent Application And Power Of Attorney, submitted with the

above-captioned 35 U.S.C. 371 national application. Accordingly, no new matter is added, and entry of the amendment is respectfully requested.

The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: February 11, 2002

Jason I. Garbell, Reg. No. 44,116
Novozymes North America, Inc.
405 Lexington Avenue, Suite 6400
New York, NY 10174-6401
(212) 867-0123

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MAY 03 2002
TECH CENTER 1600/2900

Attorney Docket No.: 5559.204-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bojsen et al.

Serial No.: 09/856,819

Confirmation No: To Be Assigned

Group Art Unit: To Be Assigned

Filed: May 24, 2001

Examiner: To Be Assigned

For: Lipolytic Enzyme Variants

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Sir:

Below is a marked-up version of the amendments made in the accompanying amendment.

IN THE SPECIFICATION:

The paragraph under the heading "CROSS-REFERENCE TO RELATED APPLICATIONS" has been amended as follows:

--CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a 35 U.S.C. 371 national application of PCT/DK99/00664, filed November 29, 1999, and claims, under 35 U.S.C. 119, priority of Danish application nos. PA 1998 01572, filed November 27, 1998, [PA 1998 01573, filed November 27, 1998,] PA 1999 00391, filed March 22, 1999, PA 1999 01481, filed October 15, 1999, and the benefit under 35 U.S.C. 119(e) of United States provisional patent application nos. 60/111,430, filed on December 8, 1998, 60/126,914, filed on March 29, 1999, and 60/160,735, filed on October 22, 1999, the contents of which are fully incorporated herein by reference.--

Rec'd PCT/PTO 15 OCT 2001

Attorney Docket No.: 5559.204-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bojsen et al.

Serial No.: 09/856,819

Group Art Unit: To Be Assigned

Filed: May 24, 2001

Examiner: To Be Assigned

For: Lipolytic Enzyme Variants

PRELIMINARY AMENDMENT AND RESPONSE TO NOTICE TO FILE MISSING PARTS AND TO NOTICE TO COMPLY WITH SEQUENCE RULES

Box PCT
Commissioner for Patents
Washington, DC 20231

Sir:

In response to the Notice to Comply with Sequence Rules dated July 17, 2001, please amend the above-identified application as follows (a marked up version pursuant to 37 C.F.R. 1.21 is attached hereto):

IN THE SPECIFICATION:

Please add the two attached pages to the specification at the end of page 43.

Please replace the paragraph on page 9, lines 4-9, with:

--Alternatively, the variant may carry a peptide extension at the C-terminal and/or the N-terminal. The C-terminal extension may consist of 1-10 amino acid residues, e.g. A, P, AG, DG, PG, AGG, PVGF (SEQ ID. NO. 15), AGRF (SEQ ID. NO. 16), PRGF (SEQ ID. NO. 17) , AGGF (SEQ ID. NO. 18) or AGGFS (SEQ ID. NO. 19); or it may consist of 40-50 residues, e.g., consisting of the 48 C-terminal residues of the *Fusarium oxysporum* lipase GGFSWRRYRSAESVDKRATMTDAELEKKLNSYVQMD KEYVKNNQARS (SEQ ID. NO. 20). The C-terminal extension may increase the phospholipase activity.--

Please replace the paragraph on page 10, lines 24-31, with:

--The variant of the invention may further comprise a peptide extension at the N-terminal, e.g. consisting of 1-15 (particularly 4-10) amino acid residues, and specifically comprising 1, 2 or 3 positively charged amino acids. Some specific N-terminal peptide extensions are AS, SPIRR (SEQ ID. NO. 21), E1RP, E1SPIRPRP (SEQ ID. NO. 22), E1SPPRRP (SEQ ID. NO. 23) and E1SPIRPRP (SEQ ID NO:22). Further, any peptide extension described in WO 97/04079 and WO 97/07202 may be used.--

Please replace the paragraph on page 11, lines 21-27, with:

--Specific variants of the *H. lanuginosa* lipase are disclosed in the examples. Corresponding alterations may be made in other parent lipolytic enzymes. Further variants may be derived from these by omitting amino acid modifications at positions 1, 106, 186, 225, 232, 237, 239 or 274. Variants with 274S may optionally have a further C-terminal extension of WRRYRSAESVDKRATMTDAELEKKLNSYVQM DKEYVKNNQARS (SEQ ID. NO. 24) (corresponding to the C-terminal of the *F. oxysporum* lipase) in full or truncated form.--

Please replace the paragraph on page 12, lines 1 – 6, with:

T267stop indicates a stop codon, i.e. deletion of T267 and all following amino acids (i.e. C268 and L269). 270P, 271V indicates a C-terminal extension of PV (i.e. at new positions 270 and 271). -G266 indicates deletion of G at position 266. Parentheses indicate that the alteration is optional, or in examples that the alteration is uncertain. SPIRR (SEQ ID NO:21) indicates an N-terminal extension. D266 may refer to the position or to substitution with any amino acid (except D).

Please replace the paragraph on page 12, lines 7-10, with:

--E1SPPCGRRP (SEQ ID. NO. 25) or SPPCGRRP(-E) (SEQ ID NO.25) indicates a substitution of E1 with SPPCGRRP (SEQ ID NO:25), i.e. a peptide addition at the N-terminal. T267GS indicates a substitution of T267 with GS, or in other words the substitution T267G and an insertion of S between G267 and C268.--

Please replace the paragraph on page 33, lines 15-26, with:

--The gene encoding the lipolytic enzyme in question is inserted into the plasmid pHD414. In accord-ance with the manufacturer's instructions the ScaI site of the Ampicillin gene of pHD414 is changed to a MluI site by use of the following primer:

Primer 3: AGAAATCGGGTATCCTTTCAG. (SEQ I.D. NO. 27)

The pHD414 vector comprising the lipolytic gene in question is then used as a template for DNA polymerase and oligos 7258 and 7770.

7258: 5'p gaa tga ctt ggt tga cgc gtc acc agt cac 3' (SEQ I.D. NO. 28)

(Thus changing the ScaI site found in the ampicillin resistance gene and used for cutting to a MluI site).

Primer no. 7770 was used as the selection primer.

7770: 5'p tct agc cca gaa tac tgg atc aaa tc 3'(SEQ I.D. NO 29) (Changes the ScaI site found in the *H. lanuginosa* lipase gene without changing the amino acid sequence).

Please replace the paragraph on page 37, lines 1-4, with:

SPIRR (SEQ ID NO:21), G91A, D96W, E99K, W260C, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272, G273F, (274S)

SPIRR (SEQ ID NO:21), G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Please replace the paragraph on page 38, lines 7-10, with:

SPIRR (SEQ ID NO:21), D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

SPIRR (SEQ ID NO:21), G91A, D96W, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Please replace the table under Example 5, beginning on page 41, with:

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
SPIRR (SEQ ID NO:21), G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
E1A, G91A, D96W, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N
E1A, G91A, D96W, E99K, Q249R, G266S, 270D, 271G
E1A, G91A, D96W, E99K, Q249R, G266D
E1A, G91A, D96W, E99K, Q249R, G266A, 270P, 271G
G266D
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +L93K +E99K +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +E99K +E239C +Q249R +G266D
G266A
G266W
G266V
G263Q +L264A +I265T +G266D +T267A
G263F +L264A +G266S +T267E
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G263Q +L264A +I265T +G266D +T267A
G266S
G266L
G263A +G266A
G263A +G266Y
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266S
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G263F +L264A +G266S +T267E
D62A + G266A
D62A + G266S
D96S + G266A
D96S+ G266S
D96S+ G266R
D96S+ G266W
D96S+ G266V
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A

E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ L264P+ G266S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop
G263D +L264I +I265N +G266E +T267GS
E219G +L264I +I265N +G266T +T267GL
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ E239C+ Q249R+ P256A+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G +273F (+274S)
E1A+ G91A+ D96W+ E99K+ N248T+ Q249R+ W260Q+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ E99K+ W260C+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272+ G273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G +272G +273F (+274S)
SPIRR (SEQ ID NO:21) + D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N
E1A+ G91A+ D96W+ E99K+ Q249R+ G263E+ G266D+ L269N+ 270P+ 271V+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G263A+ G266S+ L269N+ 270A+ 271G+ 272R+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ Δ266+ L269I+ 270P+ 271R+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264C+ I265N+ G266P+ T267stop
E1A+ G91A+ D96W+ E99K (+R232L)+ Q249R+ G266S+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ 270D+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264F+ Δ266+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264G+ I265G+ G266F+ T267stop
E1A+ G91A+ D96W+ E99K+ Q249R+ L264stop
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+

L269N+ 270A+ 271G
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A+ 270P+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ I265F+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269S+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269N+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ L269N+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ L267Q+ L269N
E1A+ G91A+ D96W+ E99K+ Q249R+ G263R+ I265L+ L269N+ 270P
E1A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G225R+ G266D
E1A+ G225R+ G263A+ I265V+ G266S
E1A+ G225R+ G263A+ T267A
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ I252M+ L264Q+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ G266C+ L267A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A
E1A+ D96M+ G106S+ G225R+ G266D
E1A+ D96Q+ G106S+ G225R+ G266S
E1A+ D96F+ G225R+ G266S
E1A+ D96C+ G225R+ G266T
E1A+ D96H+ G106S+ G225R+ G266S
SPIRR (SEQ ID NO:21) + D96S+ G266D
SPIRR (SEQ ID NO:21) + D96R+ G106S+ G266D
SPIRR (SEQ ID NO:21) + D96I+ G106S+ G266S
SPIRR (SEQ ID NO:21) + D96W+ K237R+ G266S
SPIRR (SEQ ID NO:21) + G266A
SPIRR (SEQ ID NO:21) + D96S+ G106S+ G225R+ G266D

SPIRR (SEQ ID NO:21) + D96Q+ G106S+ G225R+ G266A
SPIRR (SEQ ID NO:21) + D96Y+ G106S+ G225R+ G266N
SPIRR (SEQ ID NO:21) + D96C+ G106S+ G225R+ G266T
SPIRR (SEQ ID NO:21) + D96H+ T186I+ G225R+ G266S
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ L264P+ G266S
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ T267S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266S
E1SPPCGRRP (SEQ ID NO:25) + E239C+ Q249R+ P256T+ G266S+ T267A
E1SPPCGRRP (SEQ ID NO:25) + E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP (SEQ ID NO:23) + D96S+ E239C+ Q249R+ G266D
L259S
G266D
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
G266E
G263A +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266S
D96S + G266A
D96S + G266S
D96S + G266W
E1SPPCGRRP (SEQ ID NO:23) +D96S +E239C +Q249R +G263D +L264I +I265N +G266E +T267GS
E1SPPCGRRP (SEQ ID NO:23) +D96S +E239C +Q249R +L264I +I265N +G266T +T267GL
D96F +G266A
D96F +G266S
E1SPPCGRRP (SEQ ID NO:23) +E99N +E239C +Q249R +G266A

E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G266S
E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G263F +L264A +G266S +T267E
V60G +D62A +S83T +R84K +D96W +G266D
V60G +D62A +S83T +D96W +G266D
V60G +D62A +S83T +D96W +G266W
L259I
L259N
D96W +G263Q +L264A +I265T +G266D +T267A

Please replace the table beginning on page 49, below Example 7, with:

E1SPIRPRP (SEQ ID NO:22) +G91A +D96N +E99K +Q249R
E1SPCRPRP (SEQ ID NO:26) + S83T+ N94K+ D96L+ E239C+ Q249R
G266D
E1SPIRPRP (SEQ ID NO:22) +D62A +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +D62G +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +D62V +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +R84W +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +R84K +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) + K98D +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) + E99K +Q249R + 270PGLPFKRV
E1SPPCGRRP (SEQ ID NO:25) + E99N +N101S +T231K +R232G +D234G +E239C +Q249R
E1SPIRPRP (SEQ ID NO:22) +E99K +Q249R + 270PWPARLGRL
L93K +D96G
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
E1SPCRPRP +V60G +E99N +S119G +R209P +E239C +Q249R
G266A
G266E
G266V
G263Q +L264A +I265T +G266D +T267A
G266L

G263A +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266S
D96S + G266A
D96S + G266S
D96S + G266W
L264I +I265N +G266T +T267GL
E1SPPCGRRP (SEQ ID NO:25) +D96S +E239C +Q249R +L264I +I265N +G266T +T267GL
D96F +G266A
D96F +G266S
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) + D96S +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) + D96S +E239C +Q249R +G266S
D62A + S83T
E1SPPCGRRP (SEQ ID NO:25) +K98D +E99N +E239C +Q249R
T231R +N233R +270CP
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +270MD
E1SPPCGRRP (SEQ ID NO:25) + D62A +S83T +E99N +E239C +Q249R
D62A +S83T + G91A +E99K +T231R +N233R +Q249R
V60G +D62A +S83T +R84K +D96W +G266D
L259N
L259R
L259M
L259Q
SPPCGRRP(-E) (SEQ ID NO:25) +R84W +E99N +N101S +E239C +Q249R
R84W +G91A +E99K +T231R +N233R +Q249R
Y21I
Y21V
SPIRPRP(-E) (SEQ ID NO:22) +R84L +E99K +Q249R
Y21C
SPIRPRP(-E) (SEQ ID NO:22) +D62 +E99K +Q249R
D96W +G263Q +L264A +I265T +G266D +T267A +L269N +A270 +G271 +G272 +F273 +S274.

[redacted]

G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S

The following variants of the parent lipase from *Humicola lanuginosa* may also have an increased specificity for long-chain fatty acids:

SPIRPRP(-E) (SEQ ID NO:22) +V60R +D62V +L93K +E99K +Q249R
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R
SPIRPRP(-E) (SEQ ID NO:22) +E99K +Q249R +P256D
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R +P256D
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R +P256S
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96L +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96N +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96A +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96E +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96S +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96R +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96G +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96Q +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A

+271G +272G +273F +274S
SPPCGRRP(-E) (SEQ ID NO:25) +V60G +D62E +S83T +R84K +E99N +N101S +E239C +Q249R
V60G +D62E +S83T +R84K +G91A +E99K +T231R +N233R +Q249R

Please replace the table on page 53, below Example 10, with:

SPIRPRP(-E) (SEQ ID NO:22) +E99K +R195Q +R209E +Q249R
N101R +R195Q +R209E +L259S +Y261D
N101R +R195Q +R209E +L259S
N101R +L259S +Y261D
N101R +L259S
Y261D
L259S
SPIRPRP(-E) (SEQ ID NO:22) +E99K +N101R +Q249R
G263D +L264I +I265N +G266E +T267GS
Y261I
D234R
Y261K

REMARKS

Applicants enclose a paper copy and a computer readable form of a Sequence Listing. The content of the paper and of the computer readable form is the same.

The specification has been amended to provide SEQ ID NOS for the sequences disclosed therein. The specification has also been amended to include pages 55 and 56 of Danish priority patent application PA 1999 01481, filed October 15, 1999. Support for the addition of the subject matter of these two attached pages is found, *inter alia*, on pages 55 and 56 of Danish patent application PA 1999 01481, filed October 15, 1999, and in the original sequence listing submission, namely, original SEQ ID NOS. 8, 9 and 10. This submission contains no new matter.

The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: October 12, 2001

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bojsen et al. Confirmation No: To Be Assigned

Serial No.: 09/856,819 Group Art Unit: To Be Assigned

Filed: May 24, 2001 Examiner: To Be Assigned

For: Lipolytic Enzyme Variants

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Commissioner for Patents
Washington, DC 20231

Sir:

Below is a marked-up version of the amendments made in the accompanying amendment.

IN THE SPECIFICATION:

Please amend the paragraph on page 9, lines 4-9, as follows:

--Alternatively, the variant may carry a peptide extension at the C-terminal and/or the N-terminal. The C-terminal extension may consist of 1-10 amino acid residues, e.g. A, P, AG, DG, PG, AGG, PVGF (SEQ ID. NO. 15), AGRF (SEQ ID. NO. 16), PRGF (SEQ ID. NO. 17) , AGGF (SEQ ID. NO. 18) or AGGFS (SEQ ID. NO. 19); or it may consist of 40-50 residues, e.g., consisting of the 48 C-terminal residues of the *Fusarium oxysporum* lipase GGFSWRRYRSAESVDKRATMTDAELEKKLNSYVQMD KEYVKNNQARS (SEQ ID. NO. 20). The C-terminal extension may increase the phospholipase activity.--

Please amend the paragraph on page 10, lines 24-31, as follows:

--The variant of the invention may further comprise a peptide extension at the N-terminal, e.g. consisting of 1-15 (particularly 4-10) amino acid residues, and specifically comprising 1, 2 or 3 positively charged amino acids. Some specific N-terminal peptide extensions are AS, SPIRR (SEQ ID. NO. 21), E1RP, E1SPIRPRP (SEQ ID. NO. 22),

E1SPPRRP (SEQ ID. NO. 23) and E1SPIRPRP (SEQ ID NO:22). Further, any peptide extension described in WO 97/04079 and WO 97/07202 may be used.--

Please amend the paragraph on page 11, lines 21-27, as follows:

--Specific variants of the *H. lanuginosa* lipase are disclosed in the examples. Corresponding alterations may be made in other parent lipolytic enzymes. Further variants may be derived from these by omitting amino acid modifications at positions 1, 106, 186, 225, 232, 237, 239 or 274. Variants with 274S may optionally have a further C-terminal extension of WRRYRSAESVDKRATMTDAELEKKLNSYVQM DKEYVKNNQARS (SEQ ID. NO. 24) (corresponding to the C-terminal of the *F. oxysporum* lipase) in full or truncated form.--

Please amend the paragraph on page 12, lines 1 – 6, as follows:

T267stop indicates a stop codon, i.e. deletion of T267 and all following amino acids (i.e. C268 and L269). 270P, 271V indicates a C-terminal extension of PV (i.e. at new positions 270 and 271). -G266 indicates deletion of G at position 266. Parentheses indicate that the alteration is optional, or in examples that the alteration is uncertain. SPIRR (SEQ ID NO:21) indicates an N-terminal extension. D266 may refer to the position or to substitution with any amino acid (except D).

Please amend the paragraph on page 12, lines 7-10, as follows:

--E1SPPCGRRP (SEQ ID. NO. 25) or SPPCGRRP(-E) (SEQ ID NO.25) indicates a substitution of E1 with SPPCGRRP (SEQ ID NO:25), i.e. a peptide addition at the N-terminal. T267GS indicates a substitution of T267 with GS, or in other words the substitution T267G and an insertion of S between G267 and C268.--

Please amend the paragraph on page 33, lines 15-26, as follows:

--The gene encoding the lipolytic enzyme in question is inserted into the plasmid pHD414. In accord-ance with the manufacturer's instructions the ScaI site of the Ampicillin gene of pHD414 is changed to a MluI site by use of the following primer:

Primer 3: AGAAATCGGGTATCCTTTCAG. (SEQ I.D. NO. 27)

[redacted]

The pHD414 vector comprising the lipolytic gene in question is then used as a template for DNA polymerase and oligos 7258 and 7770.

7258: 5'p gaa tga ctt ggt tga cgc gtc acc agt cac 3' (SEQ I.D. NO. 28)

(Thus changing the ScaI site found in the ampicillin resistance gene and used for cutting to a MluI site).

Primer no. 7770 was used as the selection primer.

7770: 5'p tct agc cca gaa tac tgg atc aaa tc 3'(SEQ I.D. NO 29) (Changes the ScaI site found in the *H. lanuginosa* lipase gene without changing the amino acid sequence).

Please amend lines 1-4 on page 37, as follows:

SPIRR (SEQ ID NO:21), G91A, D96W, E99K, W260C, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272, G273F, (274S)

SPIRR (SEQ ID NO:21), G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Please amend lines 7-10 on page 38, as follows:

SPIRR (SEQ ID NO:21), D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

SPIRR (SEQ ID NO:21), G91A, D96W, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Please amend the table under Example 5, beginning on page 41, as follows:

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
SPIRR (SEQ ID NO:21), G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
E1A, G91A, D96W, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N
E1A, G91A, D96W, E99K, Q249R, G266S, 270D, 271G
E1A, G91A, D96W, E99K, Q249R, G266D

E1A, G91A, D96W, E99K, Q249R, G266A, 270P, 271G
G266D
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +L93K +E99K +E239C +Q249R +G266D
E1SPPCGRRP (SEQ ID NO:25) +E99K +E239C +Q249R +G266D
G266A
G266W
G266V
G263Q +L264A +I265T +G266D +T267A
G263F +L264A +G266S +T267E
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G263Q +L264A +I265T +G266D +T267A
G266S
G266L
G263A +G266A
G263A +G266Y
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G266S
E1SPPCGRRP (SEQ ID NO:25) +E239C +Q249R +G263F +L264A +G266S +T267E
D62A + G266A
D62A + G266S
D96S + G266A
D96S+ G266S
D96S+ G266R
D96S+ G266W
D96S+ G266V
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ L264P+ G266S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop

[redacted]

G263D +L264I +I265N +G266E +T267GS
E219G +L264I +I265N +G266T +T267GL
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ E239C+ Q249R+ P256A+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G +273F (+274S)
E1A+ G91A+ D96W+ E99K+ N248T+ Q249R+ W260Q+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ E99K+ W260C+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272+ G273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G +272G +273F (+274S)
SPIRR (SEQ ID NO:21) + D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR (SEQ ID NO:21) + G91A+ D96W+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N
E1A+ G91A+ D96W+ E99K+ Q249R+ G263E+ G266D+ L269N+ 270P+ 271V+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G263A+ G266S+ L269N+ 270A+ 271G+ 272R+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ Δ266+ L269I+ 270P+ 271R+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264C+ I265N+ G266P+ T267stop
E1A+ G91A+ D96W+ E99K (+R232L)+ Q249R+ G266S+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ 270D+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264F+ Δ266+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264G+ I265G+ G266F+ T267stop
E1A+ G91A+ D96W+ E99K+ Q249R+ L264stop
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D

E1A+ G91A+ D96W+ E99K+ Q249R+ G266D
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A+ 270P+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ I265F+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269S+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269N+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ L269N+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ L267Q+ L269N
E1A+ G91A+ D96W+ E99K+ Q249R+ G263R+ I265L+ L269N+ 270P
E1A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G225R+ G266D
E1A+ G225R+ G263A+ I265V+ G266S
E1A+ G225R+ G263A+ T267A
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ I252M+ L264Q+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + D96S+ E239C+ Q249R+ G266C+ L267A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A
E1A+ D96M+ G106S+ G225R+ G266D
E1A+ D96Q+ G106S+ G225R+ G266S
E1A+ D96F+ G225R+ G266S
E1A+ D96C+ G225R+ G266T
E1A+ D96H+ G106S+ G225R+ G266S
SPIRR (SEQ ID NO:21) + D96S+ G266D
SPIRR (SEQ ID NO:21) + D96R+ G106S+ G266D
SPIRR (SEQ ID NO:21) + D96I+ G106S+ G266S
SPIRR (SEQ ID NO:21) + D96W+ K237R+ G266S
SPIRR (SEQ ID NO:21) + G266A
SPIRR (SEQ ID NO:21) + D96S+ G106S+ G225R+ G266D
SPIRR (SEQ ID NO:21) + D96Q+ G106S+ G225R+ G266A
SPIRR (SEQ ID NO:21) + D96Y+ G106S+ G225R+ G266N
SPIRR (SEQ ID NO:21) + D96C+ G106S+ G225R+ G266T
SPIRR (SEQ ID NO:21) + D96H+ T186I+ G225R+ G266S

[redacted]

E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ L264P+ G266S
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPRRP (SEQ ID NO:23) + G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ T267S
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ P256T+ G266S
E1SPPCGRRP (SEQ ID NO:25) + E239C+ Q249R+ P256T+ G266S+ T267A
E1SPPCGRRP (SEQ ID NO:25) + E239C+ Q249R+ G266D
E1SPPCGRRP (SEQ ID NO:25) + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP (SEQ ID NO:23) + D96S+ E239C+ Q249R+ G266D
L259S
G266D
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
G266E
G263A +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266S
D96S + G266A
D96S + G266S
D96S + G266W
E1SPPCGRRP (SEQ ID NO:23) +D96S +E239C +Q249R +G263D +L264I +I265N +G266E +T267GS
E1SPPCGRRP (SEQ ID NO:23) +D96S +E239C +Q249R +L264I +I265N +G266T +T267GL
D96F +G266A
D96F +G266S
E1SPPCGRRP (SEQ ID NO:23) +E99N +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G266S
E1SPPCGRRP (SEQ ID NO:23) + D96S +E239C +Q249R +G263F +L264A +G266S +T267E
V60G +D62A +S83T +R84K +D96W +G266D

V60G +D62A +S83T +D96W +G266D
V60G +D62A +S83T +D96W +G266W
L259I
L259N
D96W +G263Q +L264A +I265T +G266D +T267A

Please amend the table beginning on page 49, below Example 7, as follows:

E1SPIRPRP (SEQ ID NO:22) +G91A +D96N +E99K +Q249R
E1SPCRPRP (SEQ ID NO:26) + S83T+ N94K+ D96L+ E239C+ Q249R
G266D
E1SPIRPRP (SEQ ID NO:22) +D62A +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +D62G +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +D62V +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +R84W +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) +R84K +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) + K98D +E99K +Q249R
E1SPIRPRP (SEQ ID NO:22) + E99K +Q249R + 270PGLPFKRV
E1SPPCGRRP (SEQ ID NO:25) + E99N +N101S +T231K +R232G +D234G +E239C +Q249R
E1SPIRPRP (SEQ ID NO:22) +E99K +Q249R + 270PWPARLGRL
L93K +D96G
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
E1SPCRPRP +V60G +E99N +S119G +R209P +E239C +Q249R
G266A
G266E
G266V
G263Q +L264A +I265T +G266D +T267A
G266L
G263A +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266A
E1SPCRPRP (SEQ ID NO:26) +E239C +Q249R +G266S
D96S + G266A

D96S + G266S
D96S + G266W
L264I +I265N +G266T +T267GL
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D96F +G266A
D96F +G266S
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) + D96S +E239C +Q249R +G266A
E1SPPCGRRP (SEQ ID NO:25) + D96S +E239C +Q249R +G266S
D62A + S83T
E1SPPCGRRP (SEQ ID NO:25) +K98D +E99N +E239C +Q249R
T231R +N233R +270CP
E1SPPCGRRP (SEQ ID NO:25) +E99N +E239C +Q249R +270MD
E1SPPCGRRP (SEQ ID NO:25) + D62A +S83T +E99N +E239C +Q249R
D62A +S83T + G91A +E99K +T231R +N233R +Q249R
V60G +D62A +S83T +R84K +D96W +G266D
L259N
L259R
L259M
L259Q
SPPCGRRP(-E) (SEQ ID NO:25) +R84W +E99N +N101S +E239C +Q249R
R84W +G91A +E99K +T231R +N233R +Q249R
Y21I
Y21V
SPIRPRP(-E) (SEQ ID NO:22) +R84L +E99K +Q249R
Y21C
SPIRPRP(-E) (SEQ ID NO:22) +D62 +E99K +Q249R
D96W +G263Q +L264A +I265T +G266D +T267A +L269N +A270 +G271 +G272 +F273 +S274.
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S

The following variants of the parent lipase from *Humicola lanuginosa* may also have an increased specificity for long-chain fatty acids:

SPIRPRP(-E) (SEQ ID NO:22) +V60R +D62V +L93K +E99K +Q249R
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R
SPIRPRP(-E) (SEQ ID NO:22) +E99K +Q249R +P256D
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R +P256D
SPIRPRP(-E) (SEQ ID NO:22) +D62V +E99K +Q249R +P256S
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96L +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96N +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
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G91A +D96R +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
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R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
SPPCGRRP(-E) (SEQ ID NO:25) +V60G +D62E +S83T +R84K +E99N +N101S +E239C +Q249R
V60G +D62E +S83T +R84K +G91A +E99K +T231R +N233R +Q249R

Please amend the table on page 53, below Example 10, as follows:

SPIRPRP(-E) (SEQ ID NO:22) +E99K +R195Q +R209E +Q249R
N101R +R195Q +R209E +L259S +Y261D
N101R +R195Q +R209E +L259S
N101R +L259S +Y261D
N101R +L259S
Y261D
L259S
SPIRPRP(-E) (SEQ ID NO:22) +E99K +N101R +Q249R
G263D +L264I +I265N +G266E +T267GS
Y261I
D234R
Y261K

[redacted]

Primers

4244 (SEQ ID NO: 1): 5'-TCA AGA ATA GTT CAA ACA AGA AGA-3'

AP (SEQ ID NO: 2): 5'-GGT TGT CTA ACT CCT TCC TTT TCG-3'

FOL14 (SEQ ID NO: 3): 5'-TGT CCC YMG WCT CCC KCC K-3'

FOL15 (SEQ ID NO: 4): 5'-GAA GTA MYR YAG RTG MGC AGS RAT ATC-3'

FOL16 (SEQ ID NO: 5): 5'-GAT ATY SCT GCK CAY CTR YRK TAC TTC-3'

H7 (SEQ ID NO: 6): 5'-CGG AAT GTT AGG CTG GTT ATT GC-3'

KBoj 14 (SEQ ID NO: 7): 5'-CTT TTC GGT TAG AGC GGA TG-3'

KBoj 32 (SEQ ID NO: 8): GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA 122 345 345 S67 C8A 91011 S1213 1.14.15 161718 T1920 C2122 GAA GTA CCA TAG GTG CGC AG23 GAT ATC CGG

KBoj 33: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CGC CGC GCA CTA C8A 91011 S1213 1.14.15 161718 T1920 C2122 GAA GTA CCA TAG GTG CGC AG23 GAT ATC CGG

KBoj34: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA 122 345 345 S67 201818 91011 S1213 1.14.15 161718 T1920 C2122 GAA GTA CCA TAG GTG CGC AG23 GAT ATC CGG

KBoj36: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA GTT ACA GGC GTC AGT CGC CTG GAA G

KBoj37: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA AGC GTT ACA GGC GTC AGT CGC CTG G

KBoj38: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA ACC AGC GTT ACA GGC GTC AGT CGC C

KBoj39: GTA AGC GTG ACA TAA CTA ATT ACA TCA TGC GGC CCT CTA GAG TCG ACC CAG CCG CTA GCC ACC AGC GTT ACA GGC GTC AGT C

Distribution of nucleotides for each doped position

1: A 90, C 10

2: G 3,A 91,T 3,C 3

3: A 25, T 75

4: G 2, A 4, T 5, C 89

5: G 2, A 13, T 4, C 81

6: G 91, A 3, T 3, C 3

7: G 48, A 2, T 2, C 48

8: A 92, T8

9: A 97, T 3

10: G 1, A 1, T 1, C 97

[redacted]

11: G 1, A 97, T 1, C 1
12: G 94, A 2, T 2, C 2
13: G 1, A 1, T 91, C 7
14: G 1, A 1, T 7, C 91
15: G 2, A 2, T 2, C 94
16: A 80, T 20
17: G 6, A 90, T 2, C 2
18: G 2, A 2, T 94, C 2
19: G 5, A 91, T 4
20: G 96, C4
21: G 4, T 5, C 91
22: G 4, C 96
23: G 94, C 3, T 3

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Svendsen, Allan
Fuglsang, Claus C.
Patkar, Shamkant Anant
Borch, Kim
Vind, Jesper
Petri, Andreas
Glad, Sanne O. Schroder
Budolfsen, Gitte

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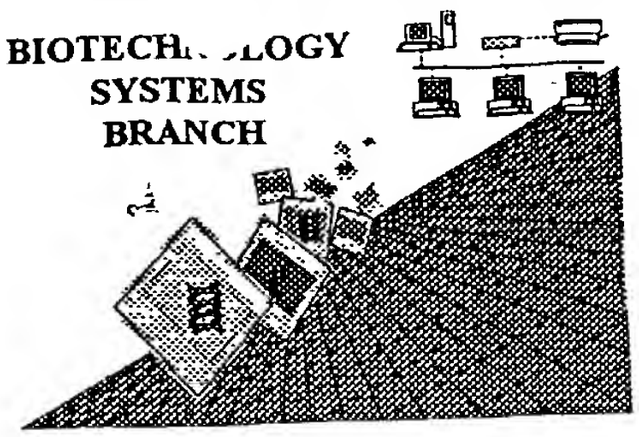

RAW SEQUENCE LISTING ERROR REPORT

BC

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Source: PCT/09

Date Processed by STIC: 6/18/2001

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

PCT09

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Does Not Comply
Corrected Diskette Needed

pr 1-5

3 <110> APPLICANT: Bojsen, Kirsten
4 Svendsen, Allan
5 Fuglsang, Claus
6 Patkar, Shamkant
7 Borch, Kim
8 Vind, Jesper
9 Petri, Andreas
10 Glad, Sanne
11 Budolfsen, Gitte
13 <120> TITLE OF INVENTION: Lipolytic Enzyme Variants
15 <130> FILE REFERENCE: 5559.204-US
C--> 17 **<140> CURRENT APPLICATION NUMBER: US/09/856,819**
C--> 18 **<141> CURRENT FILING DATE: 2001-05-24**
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RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/856,819 TIME: 16:21:20

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FYI: "n" can only represent a single nucleotide

Does this mean that "n" represents "A" 90% of instances and "C" 10% of instances?

RAW SEQUENCE LISTING DATE: 06/18/2001
PATENT APPLICATION: US/09/856,819 TIME: 16:21:20

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VERIFICATION SUMMARY DATE: 06/18/2001
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09/856819
JC18 Rec'd PCT/PTO 24 MAY 2001

Attorney Docket No.: 5559.204-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bojsen et al.

Serial No.: To Be Assigned

Confirmation No: To Be Assigned

Group Art Unit: To Be Assigned

Filed: May 24, 2001

Examiner: To Be Assigned

For: Lipolytic Enzyme Variants

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, DC 20231

Sir:

Before the above-captioned application is taken up for examination, entry of the following amendment is respectfully requested:

IN THE SPECIFICATION:

At page 1, after the title, insert

--CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a 35 U.S.C. 371 national application of PCT/DK99/00664, filed November 29, 1999, and claims, under 35 U.S.C. 119, priority of Danish application nos. PA 1998 01572, filed November 27, 1998, PA 1998 01573, filed November 27, 1998, PA 1999 00391, filed March 22, 1999, PA 1999 01481, filed October 15, 1999, the contents of which are fully incorporated herein by reference.--

IN THE CLAIMS:

Please cancel claims 1-64 without prejudice or disclaimer.

Please add the following new claims:

65. A method of producing a lipolytic enzyme variant comprising:

a) selecting a parent lipolytic enzyme having an alcohol binding site having a glycerol part with an sn2 position,

b) in the parent lipolytic enzyme, selecting at least one amino acid residue which comprises at least one atom within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride in a three-dimensional structure of the parent lipolytic enzyme and the substrate,

c) making alterations of the at least one amino acid residue,

d) preparing the variant resulting from steps a-c,

e) testing substrate specificity of the variant,

f) selecting a variant having an altered substrate specificity, and

g) producing the selected variant.

66. The method of claim 65, wherein the parent lipolytic enzyme is a lipolytic enzyme from the *Humicola* family or the *Zygomycetes* family.

67. A method of producing a lipolytic enzyme variant comprising:

a) selecting a parent lipolytic enzyme from the *Humicola* family or the *Zygomycetes* family,

b) selecting at least one amino acid residue corresponding to any of amino acids 20-25, 56-64, 81-85 and 255-269 in the *Humicola lanuginosa* lipase

c) making alterations of the at least one amino acid residue,

d) preparing the variant resulting from steps a-c,

e) testing substrate specificity of the variant, and

f) selecting a variant having an altered substrate specificity.

68. The method of claim 65, wherein the parent lipolytic enzyme is the lipase of *Humicola lanuginosa* strain DSM 4109.

69. The method of claim 65, wherein the altered substrate specificity is a lower ratio of activity towards a C_4-C_8 acyl bond in a triglyceride and a C_{16}-C_{20} acyl bond in a triglyceride.

70. The method of claim 65, wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, and the selected amino acid residues comprise an amino acid corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.

71. The method of claim 65, wherein the altered substrate specificity is a lower ratio of activity towards a C_{16}-C_{20} acyl bond in a triglyceride and a C_4-C_8 acyl bond in a triglyceride.

72. The method of claim 65, wherein the altered substrate specificity is a higher phospholipase activity.

73. The method of claim 72, wherein the parent lipolytic enzyme has a phospholipase activity below 50 PHLU/mg and/or a ratio of phospholipase activity to lipase activity below 0,1 PHLU/LU.

74. The method of claim 65, wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, and the selected amino acid residues comprise an amino acid corresponding to R81, R84, S85, or any amino acid within the range 263-267 in the *Humicola lanuginosa* lipase.

75. The method of any of claims 65, wherein the alterations comprise an insertion of a peptide extension at the C-terminal.

76. The method of any of claims 65, wherein the alterations comprise an insertion of a peptide extension at the C-terminal comprising from 1 to 5 amino acid residues.

77. The method of any of claims 65, wherein the altered activity is a higher hydrolytic activity on a digalactosyl-diglyceride.

78. The method of claim 65, wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, and the selected amino acid residues comprise an amino acid corresponding to 21, 23, 26, 57, 62, 81, 83, 84, 85, 266, 267 or 269 in the *Humicola lanuginosa* lipase.

79. An isolated lipolytic enzyme which:

a) has an amino acid sequence that is at least 80 % homologous with the amino acid sequence of a reference lipolytic enzyme of the *Humicola* family or the *Zygomycetes* family;

b) has an amino acid sequence that differs from the amino acid sequence of the reference lipolytic enzyme wherein the difference comprises:

i) an amino acid substitution, deletion or insertion at a position corresponding to A20, Y21, G23, K24, N25, V63, R81, G82, R84, A257, W260, Y261, F262 or G266 in the *Humicola lanuginosa* DSM 4109 lipase;
ii) a substitution of an amino acid corresponding to C268 or L269 in the *Humicola lanuginosa* DSM 4109 lipase;
iii) a substitution corresponding to V60G, D62E, L93K, L97Q, K98E,F, E99D, P256A, G263E,Q,R,F,N, L264A,C,P,F,G,V,I, I265L,N,F or T267A,Q,P,S,V,E in the *Humicola lanuginosa* DSM 4109 lipase;
iv) an insertion corresponding to T267GS or T267GL in the *Humicola lanuginosa* DSM 4109 lipase;
v) a peptide extension at the C-terminal which is A, P, MD, CP, AG, DG, AGG, PVGF, AGRF, PRGF, AGGF or AGGFS;
vi) a peptide extension at the C-terminal of 40-50 amino acids; or
vii) a truncation of 1, 2, 3, 4, 5 or 6 amino acids at the C-terminal.

80. The lipolytic enzyme of claim 79, wherein lipolytic enzyme has an amino acid substitution corresponding to R84K,L,W, W260H,Q,C, G266A,C,D,N,L,I,S,T,P,V,F,W,E,K,R,Y or L269N,I,S in the *Humicola lanuginosa* DSM 4109 lipase .

81. The lipolytic enzyme of claim 79, which further comprises at least one amino acid substitution, a deletion or an insertion corresponding to any of positions 22, 56-59, 61, 64, 83, 85, 91, 94, 249, 255 or 259.

82. The lipolytic enzyme of claim 79, which further comprises at least one amino acid substitution selected from the group consisting of: S83T, G91A, N94D, D96S,W,F,G, Q249R` and L259N,R,S,M,Q.

83. The lipolytic enzyme of 79, which further comprises at least one amino acid substitution selected from the group consisting of D62A,G,V, K98D, E99K, P256T, G263A or I265T,G,V.

84. The lipolytic enzyme of any of claim 79, which further comprises a peptide extension at the N-terminal compared to the reference lipolytic enzyme.

85. The lipolytic enzyme of any of claim 79, wherein the reference lipolytic enzyme is a lipase from *Humicola lanuginosa*.

86. The lipolytic enzyme of any of claim 79, wherein the reference lipolytic enzyme is alipase from *Rhizomucor miehei*.

87. The lipolytic enzyme of any of claim 79, wherein the reference lipolytic enzyme is a lipase from *Fusarium oxysporum*.

88. The lipolytic enzyme of any of claims 79, which comprises an amino acid alteration at a position corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.

89. The lipolytic enzyme of any of claim 79, which comprises an amino acid alteration at a position corresponding to R81, R84, S85, G263, L264, I265, G266, T267 or L269 in the *Humicola lanuginosa* lipase.

90. The lipolytic enzyme of any of claim 79, which comprises an amino acid substitution corresponding to G263A,E,Q,R; L264A,C,P,Q; I265L,N,T; G266A, C, D, N, L, I, S, T, P, V or T267A,Q or L269N in the *Humicola lanuginosa* lipase.

91. The lipolytic enzyme of any of claim 79, which comprises a deletion of amino acid residues at positions corresponding to positions C268 and L269 in the lipase of *Humicola lanuginosa* strain DSM 4109.

92. The lipolytic enzyme of claim 79, which comprises an alteration in the lid of the lipolytic enzyme which is a substitution of a negatively charged amino acid residue in the lid of the lipolyitc enzyme with a neutral or positively charged amino acid residue, or a substitution of a neutral amino acid residue in the lid of the lipolytic with a positively charged amino residue.

93. The lipolytic enzyme of claim 79, which comprises an alteration in the lid of the lipolyitc enzyme at a position corresponding to position G91, D96 or E99 in the *Humicola lanuginosa* lipase.

REMARKS

This amendment is submitted to cancel claims in order to reduce the filing fee and to present claims in condition suitable for United States patent practice. There is no new matter added, and entry of the amendment is respectfully requested.

This application contains a Sequence Listing. Applicants enclose a 3.5" floppy disk containing the Sequence Listing. The content of the attached paper entitled "SEQUENCE LISTING" and of the accompanying identically labeled diskette is the same.

The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: May 24, 2001

Jason I. Garbell, Reg. No. 44,116
Novozymes North America, Inc.
405 Lexington Avenue, Suite 6400
New York, NY 10174-6401
(212) 867-0123

LIPOLYTIC ENZYME VARIANTS

FIELD OF THE INVENTION

The present invention relates to a method of altering the substrate specificity of a lipolytic enzyme by modifying the amino acid sequence, and to lipolytic enzyme variants obtained by such modification. The invention also relates to a screening method for lipolytic enzymes.

BACKGROUND OF THE INVENTION

Lipolytic enzymes (such as lipases and phospholipases) are capable of hydrolyzing carboxylic ester bonds in a substrate to release carboxylic acids. The hydrolytic activity on different ester bonds is important for the usefulness of the lipolytic enzyme in various industrial applications.

Thus, enzymes with a high phospholipase activity are useful in a wide range of applications such as baking (US 4,567,046), filtration of wheat starch hydrolysate (US 5,264,367) and treatment of vegetable oil to reduce the content of phospholipid (US 5,264,367). For the treatment of vegetable oil, the enzyme should have a low lipase activity, i.e. a low hydrolytic activity towards ester bonds in triglycerides..

WO 98/45453 indicates that an enzyme with a high hydrolytic activity on digalactosyl diglyceride (DGDG) is useful in baking.

It is well known to add a lipase to laundry detergents to aid in the removal of greasy soils (e.g. EP 258,068).

The release of short-chain fatty acids as free fatty acids (FFA) may be desirable for flavor development in food products, e.g. in cheese ripening (M. Hanson, ZFL, 41 (10), 664-666 (1990)).

The three-dimensional (3D) structure of several lipolytic enzymes is known, and several structures are known to contain a so-called "lid" which may be in an open or closed state covering the active site. Brady et al., Nature, 343, 767-770 (1990). Brzozowski A M et al., Nature, 351, 491 (1991). Derewenda et al., Biochemistry, 31 (5), 1532-1541 (1992).

F. Hara et al., JAOCS, 74 (9), 1129-32 (1997) indicates that some lipases have a certain phospholipase activity, whereas most lipases have little or no activity on phospholipids. Thus, phospholipase activity has been described in the lipases from guinea pig pancreas, *Fusarium oxysporum* and *Staphylococcus hyicus*, and attempts have been made to relate the phospholipase activity to the structure of the

lipase. WO 98/26057; M.D. van Kampen et al., Chemistry and Physics of Lipids, 93 (1998), 39-45; A. Hjorth et al., Bio- chemistry 1993, 32, 4702-4707.

The prior art has described the effect on chain-length selectivity by amino acid substitutions in a lipase from *Rhizopus delemar*. Thus, R. D. Joerger et al., Lipids, 29 (6), 377-384 (1994) indicates that the variants F95D, F112W and V209W have an altered preference to C_4 and C_8 acids. R. R. Klein et al., JAOCS, 74 (11), 1401-1407 (1997) shows that the variant V206T+F95D has a higher selectivity for C_8 acid. R. R. Klein et al., Lipids, 32 (2), 123-130 (1997) indicates that the variants V209W+F112W, V94W and F95D+F214R have a higher hydrolytic activity towards C_4 and C_8 acids, and suggests that structural determinants for medium-chain length specificity may reside in the distal end of the acyl binding groove.

SUMMARY OF THE INVENTION

The inventors have found that the substrate specificity of a lipolytic enzyme can be modified by making alterations to the amino acid sequence in a defined region of the lipolytic enzyme, so as to increase the level of a desired activity or to decrease the level of an undesired activity. Thus, the inventors have developed lipolytic enzymes with a modified amino acid sequence (hereinafter called lipolytic enzyme variants, or variants for short) with a substrate specificity which can be tailored for specific uses.

Accordingly,the invention provides a method of producing a lipolytic enzyme variant and lipolytic enzyme variants prepared by the method. The method comprises:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme,

c) selecting at least one amino acid residue in a region near the active site, near the C-terminal or in the lid region of the parent lipolytic enzyme as described below,

d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),

f) preparing the resulting variant,

g) testing the activity of the variant on the ester bond in the substrate, and

h) selecting a variant having an altered activity on the ester bond.

Thus, in one aspect, the parent lipolytic enzyme has an alcohol binding site having a glycerol part with an sn2 position, and the amino acid alteration is within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride.

In another aspect, the parent lipolytic enzyme has a structure comprising a catalytic triad consisting of an active Ser, an active Asp and an active His residue, and the amino acid to be altered is either located between the active His residue of the catalytic residue and the C-terminal, or belongs to a set E defined by the following steps:

i) aligning the structure of the lipolytic enzyme with *Rhizomucor miehei* lipase structure 4TGL comprising a catalytic triad and an inhibitor phosphorus atom (4TGL-inhP), so as to minimize the sum of squares of deviation between atoms of the catalytic triads of the two structures,

ii) defining a set A consisting of atoms of the lipolytic enzyme inside a sphere of radius 18 Å with center at 4TGL-inhP,

iii) forming a first plane defined by 4TGL-inhP, the Cα atom of the active Ser residue of the parent lipolytic enzyme, and the Cα atom of the active Asp residue of the parent lipolytic enzyme and defining a set B as a subset of set A consisting of atoms on the same side of the first plane as the Cα atom of the active His residue of the parent lipolytic enzyme,

iv) forming a second plane defined by 4TGL-inhP, the Cα atom of the active Ser residue of the parent lipolytic enzyme, and the Cα atom of the active His residue of the parent lipolytic enzyme and defining a set C as a subset of set A consisting of atoms on the opposite side of the second plane from the Cα atom of the active Asp residue of the parent lipolytic enzyme,

v) forming a set D consisting of atoms belonging to the union of sets B and C, and having a solvent accessibility of 15 or higher, and

vi) forming set E consisting of amino acid residues in the structure which comprise an atom belonging to set D or an atom belonging to the union of sets B and C and located less than 3.5 Å from an atom belonging to set D,

In a third aspect, the lipolytic enzyme has an active site comprising an active His residue, and the alteration is made in the amino acid sequence between the active His residue and the C-terminal.

In yet another aspect of the invention, the amino acid alteration is made among the 10 amino acid residues at the C-terminal.

In a further aspect, the parent lipolytic enzyme has a lid, and the alteration is made in the lid.

The invention also provides a DNA sequence encoding the variant, an expression vector comprising the DNA sequence, a transformed host cell harboring the DNA sequence or the expression vector, and to a method of producing the variant by cultivating the transformed host cell so as to produce the variant and recovering the variant from the resulting broth. Further, the invention provides uses of the variants.

The inventors have also found that a lipolytic enzyme which has lipase and phospholipase activity as well as activity on digalactosyl diglyceride is particularly effective for use in baking, and they designed a screening method for lipolytic enzymes by testing for these activities.

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 shows an alignment of lipase sequences.

DETAILED DESCRIPTION OF THE INVENTION

Altered activity on selected ester bond in substrate

Compared to the parent lipolytic enzyme, the invention aims to alter the activity on at least one selected ester bond in at least one substrate, i.e. to increase a desired activity, decrease an undesired activity or to change the substrate specificity by decreasing the ratio of an undesired activity to a desired activity.

Thus, an enzyme with increased phospholipase activity may be useful, e.g., in baking or in purification of vegetable oil. It may be desired to increase the hydrolytic activity on digalactosyl-diglyceride (DGDG) for use in baking.

It may be desired to increase the lipase activity for any industrial use where lipases are used. For use in detergents or baking it may be desired to increase the activity on long-chain (C_{16}-C_{20}) triglycerides, and it may be desired to increase the specificity for long-chain fatty acids by decreasing the ratio of activity on short-chain or medium-chain (C_4-C_8) fatty acids to the activity on long-chain fatty acids.

For use in, or for use in flavor development in food products (such as cheese ripening) it may be desired to increase the lipase activity on short-chain or medium-chain (C_4-C_8) triglycerides.

For use as a phospholipase in purification of vegetable oil, it may be desired to decrease the ratio of lipase activity on long-chain (C_{16}-C_{20}) triglycerides to the phospholipase activity.

Parent lipolytic Enzyme

The lipolytic enzyme to be used in the present invention is one that can hydrolyze ester bonds. Such enzymes include, for example, lipases, such as triacylglycerol lipase (EC 3.1.1.3), lipoprotein lipase (EC 3.1.1.34), monoglyceride lipase (EC 3.1.1.23), lysophospholipase, ferulic acid esterase and esterase (EC 3.1.1.1, EC 3.1.1.2). The numbers in parentheses are the systematic numbers assigned by the Enzyme Commission of the International Union of Biochemistry in accordance with the type of the enzymatic reactivity of the enzyme.

The parent lipolytic enzyme may be prokaryotic, particularly a bacterial enzyme, e.g. from *Pseudomonas*. Examples are *Pseudomonas* lipases, e.g. from *P. cepacia* (US 5,290,694, pdb file 1OIL), *P. glumae* (N Frenken et al. (1992), Appl. Envir. Microbiol. 58 3787-3791, pdb files 1TAH and 1QGE), *P. pseudoalcaligenes* (EP 334 462) and *Pseudomonas sp.* strain SD 705 (FERM BP-4772) (WO 95/06720, EP 721 981, WO 96/27002, EP 812 910). The *P. glumae* lipase sequence is identical to the amino acid sequence of *Chromobacterium viscosum* (DE 3908131 A1). Other examples are bacterial cutinases, e.g. from *Pseudomonas* such as *P. mendocina* (US 5,389,536) or *P. putida* (WO 88/09367).

Alternatively, the parent lipolytic enzyme may be eukaryotic, e.g. a fungal lipolytic enzyme such as lipolytic enzymes of the *Humicola* family and the *Zygomycetes* family and fungal cutinases.

Examples of fungal cutinases are the cutinases of *Fusarium solani pisi* (S. Longhi et al., Journal of Molecular Biology, 268 (4), 779-799 (1997)) and *Humicola insolens* (US 5,827,719).

The *Humicola* family of lipolytic enzymes consists of the lipase from *H. lanuginosa* strain DSM 4109 and lipases having more than 50 % homology with said lipase. The lipase from *H. lanuginosa* (synonym *Thermomyces lanuginosus*) is described in EP 258 068 and EP 305 216, and has the amino acid sequence shown in positions 1-269 of SEQ ID NO: 2 of US 5,869,438.

The *Humicola* family also includes the following lipolytic enzymes: lipase from *Penicillium camembertii* (P25234), lipase/phospholipase from *Fusarium oxysporum* (EP 130064, WO 98/26057), lipase from *F. heterosporum* (R87979), lysophospholipase from *Aspergillus foetidus* (W33009), phospholipase A1 from *A. oryzae* (JP-A 10-155493), lipase from *A. oryzae* (D85895), lipase/ferulic acid es-

terase from *A. niger* (Y09330), li- pase/ferulic acid esterase from *A. tubingensis* (Y09331), lipase from *A. tubingensis* (WO 98/45453), lysophospholipase from *A. niger* (WO 98/31790), lipase from *F. solanii* having an isoelectric point of 6.9 and an apparent molecular weight of 30 kDa (WO 96/18729).

The *Zygomycetes* family comprises lipases having at least 50 % homology with the lipase of *Rhizomucor miehei* (P19515). This family also includes the lipases from *Absidia reflexa*, *A. sporophora*, *A. corymbifera*, *A. blakesleeana*, *A. griseola* (all described in WO 96/13578 and WO 97/27276) and *Rhizopus oryzae* (P21811). Numbers in parentheses indicate publication or accession to the EMBL, GenBank, GeneSeqp or Swiss-Prot databases.

It is of particular interest to derive a variant with phospholipase activity from a parent lipolytic enzyme having no or very little phospholipase activity, e.g. corresponding to a ratio of phospholipase activity to lipase activity below 0.1 PHLU/LU or below 50 PHLU/mg.

Alteration near alcohol binding site

As already stated, the amino acid sequence of the parent lipolytic enzyme may be modified at a position which near the glycerol part of a substrate triglyceride. This region will be referred to as the "alcohol binding site" of the lipase; it is described in Brzozowski A M et al., Nature, 351: 491 (1991); Uppenberg et al., Biochemistry, 1995, 34, 16838-16851; A. Svendsen, Inform, 5(5), 619-623 (1994).

For the *Rhizomucor miehei* lipase, the extent of the alcohol binding site can be found from the PDB file "5tgl.pdb" available in Structural Classification of Proteins (SCOP) on the Internet, at http://www.rcsb.org/pdb/, showing the complex with the inhibitor n-hexylphosphonate ethyl ester which mimics the substrate. It is described in Derewenda et al. (supra), Brzozowski et al. (supra) and Brady et al. (supra). The sn2 position of this model is the atom CE2.

The variant typically contains no more than 10 alterations in the alcohol binding site, e.g. 1, 2, 3, 4, 5 or 6 alterations.

The alteration may particularly be in that part of the alcohol binding site which comes within 20 positions (e.g. within 10 positions) of the C-terminal.

As already stated, the amino acid sequence of the parent lipolytic enzyme may be modified at a position which is within 10 Å (e.g. within 8 Å, particularly within 6 Å) of the C atom at the sn2 position of the glycerol part of a substrate triglyceride. The following amino acid positions lie within 10 Å of the sn2 position in the *Rhizomucor miehei* lipase: 25, 28, 80-84, 88, 143-146, 175, 203, 205, 254-255, 257-259, 264-

267. The following are within 8 Å: 81-83, 144, 257-258, 265-267, and the following within 6 Å: 82, 144, 257, 266.

In the *Humicola lanuginosa* lipase, the following positions are within 10 Å of the sn2 position: 18, 21, 81-85, 89, 145-148, 172, 201, 203, 255-256, 258-260, 264-267. The following are within 8 Å: 82-84, 89, 146, 258-259, 265-267, and the following within 6 Å: 83, 146, 258, 266.

Alteration near catalytic triad

As already stated, in one aspect the parent lipolytic enzyme has a structure comprising a catalytic triad consisting of an active Ser, an active Asp and an active His residue, and the amino acid to be altered belongs to a set defined by a certain procedure described above. The structure may be an open or a closed structure, and it may or may not include a substrate or an inhibitor.

The procedure is conveniently performed by use of software such as MSI's Insight II. It involves alignment with 4TGL, a crystal structure of the lipase from *Rhizomucor miehei* inhibited irreversibly by diethyl p-nitrophenyl phosphate. This is available in Structural Classification of Proteins (SCOP) on the Internet, at http://www.rcsb.org/pdb/, and is described in Derewenda et al. (supra). The *Rhizomucor miehei* lipase comprises a catalytic triad consisting of the amino acid residues S144, D203 and H 257.

For the *Humicola lanuginosa* lipase, the structure 1tib may be used; it is available in Structural Classification of Proteins (SCOP) on the Internet. Using this structure, the set defined by the procedure includes the following positions: 10-23, 26, 40, 55-64, 80-87, 116-117, 119, 145-149, 151, 168, 170, 194, 196-201, 220-222, 224-227, and 254-269.

Alteration between at C-terminal side of the active His residue

As stated above, one or more alterations may be made in the amino acid sequence between an active His residue and the terminal, specifically among the 12 amino acids at the C-terminal side of the active His.

The *Humicola lanuginosa* lipase has an active His at H258 and the C-terminal at L269, so this region includes positions 259-269. The *P. cepacia* lipase has an active H286 and the C-terminal at residue 297, so the region includes residues 287-297.

Alteration near C-terminal

As stated above, one or more alterations may be made within 10 amino acid positions from the C-terminal of the mature protein,

or at positions corresponding to such positions in the *H. lanuginosa* lipase, i.e. positions 260-269 of the *H. lanuginosa* lipase. Corresponding positions may be found by alignment of the two sequences as described later in this specification.

The lipolytic enzyme variant may be truncated by deleting amino acid residues corresponding to the first 1, 2, 3, 4, 5 or 6 positions at the C-terminal. A truncated variant may have improved thermostability.

Alternatively, the variant may carry a peptide extension at the C-terminal and/or the N-terminal. The C-terminal extension may consist of 1-10 amino acid residues, e.g. A, P, AG, DG, PG, AGG, PVGF, AGRF, PRGF, AGGF or AGGFS; or it may consist of 40-50 residues, e.g., consisting of the 48 C-terminal residues of the *Fusarium oxysporum* lipase AGGFSWRRYRSAESVDKRATMTDAELEKKLNSYVQMDKEYVKNNQARS. The C-terminal extension may increase the phospholipase activity.

Some alterations in the region overlapping with the alcohol binding site are described below.

A specific alteration is a substitution at a position corresponding to G266 in the *Humicola lanuginosa* lipase, specifically with an amino acid of intermediate size, e.g. A, C, D, N, L, I, S, T, P or V. Such alteration alone has been found sufficient to increase the phospholipase activity.

Other specific alterations are such that alter the tertiary structure, e.g. by introducing bulky side chains or by disrupting the bond angles, e.g. by introducing Pro. Such alterations may be made at positions corresponding to positions G263, L264, I265, T267 or L269 in the *Humicola lanuginosa* lipase. Some specific substitutions are G263A,E,Q,R; L264A,C,P,Q; I265L,N,T; T267A,Q or L269N.

Alteration in lid

As stated above, the amino acid sequence of the prent lipolytic enzyme may be modified in the lid region of the parent lipolytic enzyme. This region is described in Brady et al., Nature 343, 1990, pp. 767-770 and in Brzozowski A M et al., Nature, 351: 491 (1991). In the *H. lanuginosa* lipase, the lid is located at positions 80-100, and the modification may particularly be made at positions 82-98, e.g. 91-98.

The variant typically contains no more than 5 alterations in the lid region; it may contain 0, 1, 2 or 3 alterations. A specific alteration is a substitution of an amino acid corresponding to G91, L93, N94, D96, K98, L97 and/or E99 in the *Humicola lanu-*

ginosa lipase with a neutral or positively charged amino acid, e.g. a substitution corresponding to G91A,T, L93K, N94D, D96S,W,G, L97Q, K98D,F,E and/or E99K,D.

Specifically, a variant with an alteration in the lid region also contains one or more alterations near the catalytic triad, near the substrate binding site or near the C-terminal.

Lipolytic enzyme variants

The lipolytic enzyme variant of the invention comprises one or more alterations of an amino acid residue in any of the regions described above. Each alteration may be a deletion or a substitution of the amino acid residue, or it may be an insertion before or after the amino acid residue. If the amino acid residue is at the C-terminal, the insertion may be a C-terminal extension. An insertion typically consists of 1-5 amino acid residues, e.g. 1-2, and a C-terminal extension may consist of 1-50 or 2-10 amino acid residues.

The total number of alterations in the above regions is typically not more than 20, e.g. not more than 10 or not more than 5, and there may be as little as 1 or 2 alterations in the above regions.

In addition, the lipolytic enzyme variant of the invention may optionally include other modifications of the parent enzyme, typically not more than 10, e.g. not more than 5 such modifications.

The variant generally has a homology with the parent lipolytic enzyme of at least 80 %, e.g. at least 85 %, typically at least 90 % or at least 95 %.

The variant of the invention may further comprise a peptide extension at the N-terminal, e.g. consisting of 1-15 (particularly 4-10) amino acid residues, and specifically comprising 1, 2 or 3 positively charged amino acids. Some specific N-terminal peptide extensions are AS, SPIRR, E1RP, E1SPIRPRP, E1SPPRRP and E1SPIRPRP. Further, any peptide extension described in WO 97/04079 and WO 97/07202 may be used.

Specific variants

To prepare variants of a lipolytic enzyme of the *Humicola* family, the amino acid alterations may specifically be made at positions corresponding to 20-25, 56-64, 81-85 or 255-269 in the *Humicola lanuginosa* lipase. Thus, the alteration may be a substitution, deletion or insertion at a position corresponding to A20, Y21, G23, K24, N25, V63, R81, G82, R84, A257, W260, Y261, F262 or G266 (e.g. excluding G23C, K24C, R81C), a substitution of an amino acid corresponding to C268 or L269.

Some specific alterations are substitutions corresponding to the following in *H.* lanuginosa lipase: Y21V/I/L/A/G/M/W/P/F/N/Q/S/T, V60V/I/L/A/G/M/W/P/F/N/Q/S/T, G61V/I/L/A/G/M/W/P/F/N/Q/S/T, D62E/A/V, S83T, R84K/L/W, P256A, G263E,Q,R,F, L264A,C,P,F,G,I, I265L,N,F G266D/E or T267A,Q,P,S,E, or an insertion corresponding to T267GS or T267GL.

To alter the activity towards short-chain (C_4-C_8) fatty acids in triglycerides, alterations may be made at positions corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266, e.g. a substitution corresponding to Y21V/I, V60G, D62E/A/V, S83T, R84K/L/W or G266D/E.

To increase the activity for DGDG, alterations may be made at positions corresponding to Y21, G23, N26, D57, D62, R81, S83, R84, S85, G266, T267 or L269; e.g., two or more such alterations may be made, e.g. together with one or more alterations in the lid region. To increase the phospholipase activity, alterations may be made at positions corresponding to R81, R84, S85, or 263-267, e.g. G266 or T267.

To prepare variants of a *Pseudomonas* lipase, amino acid modifications may be made at positions corresponding to 12-13, 16-34, 45-52, 59-66, 68, 86-87, 107-109, 111, 143-153, 155, 157-158, 207-212, 228, 230, 242-249, 264, 279-280, 282-297, 301-302, 304-305, 307-308 in the *P. cepacia* lipase, particularly L17/L17, T18/A18, Y29/Y29, L287/L286, E289/E288, I290/I289, Q292/Q291 or L293/L292 in the *P. cepacia*/*P. glumae* lipase.

Specific variants of the *H. lanuginosa* lipase are disclosed in the examples. Corresponding alterations may be made in other parent lipolytic enzymes. Further variants may be derived from these by omitting amino acid modifications at positions 1, 106, 186, 225, 232, 237, 239 or 274. Variants with 274S may optionally have a further C-terminal extension of WRRYR-SAESVDKRATMTDAELEKKLNSYVQMDKEYVKNNQARS (corresponding to the C-terminal of the *F. oxysporum* lipase) in full or truncated form.

Nomenclature for amino acid alterations

The nomenclature used herein for defining mutations is basically as described in WO 92/05249. Thus, G91A indicates substitution of G in position 91 with A. T267A,Q indicates substitution of T at position 267 with A or Q. E1E,D,A indicates that E1 is unchanged or is substituted with D or A.

T267stop indicates a stop codon, i.e. deletion of T267 and all following amino acids (i.e. C268 and L269). 270P, 271V indicates a C-terminal extension of PV (i.e. at new positions 270 and 271). -G266 indicates deletion of G at position 266. Parentheses indicate that the alteration is optional, or in examples that the alteration

is uncertain. SPIRR indicates an N- terminal extension. D266 may refer to the position or to substitution with any amino acid (except D).

E1SPPCGRRP or SPPCGRRP(- E) indicates a substitution of E1 with SPPCGRRP, i.e. a peptide addition at the N-terminal. T267GS indicates a substitution of T267 with GS, or in other words the substitution T267G and an insertion of S between G267 and C268.

Homology and alignment

For purposes of the present invention, the degree of homology may be suitably determined by means of computer programs known in the art, such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711) (Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-45), using GAP with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

In the present invention, corresponding (or homologous) positions in the lipase sequences of *Rhizomucor miehei* (rhimi), *Rhizopus delemar* (rhidl), *Thermomyces lanuginosa* (former; *Humicola lanuginosa*) (SP400), *Penicillium camembertii* (Pcl) and *Fusarium oxysporum* (FoLnp11), are defined by the alignment shown in Figure 1.

To find the homologous positions in lipase sequences not shown in the alignment, the sequence of interest is aligned to the sequences shown in Figure 1. The new sequence is aligned to the present alignment in Fig. 1 by using the GAP alignment to the most homologous sequence found by the GAP program. GAP is provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711) (Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-45). The following settings are used for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

Variants with phospholipase activity

As described above, the variant of the invention may have a higher phospholipase activity than the parent lipolytic enzyme. By the monolayer method described later in this specification, the variant may have a phospholipase activity of at least 0.1 nmol/min at pH 5.

By the PHLU method described later in this specification, the variant may have a phospholipase activity of at least 100 PHLU/mg (mg of pure enzyme protein), particularly at least 500 PHLU/mg. The variant has a ratio of phospholipase activity to lipase activity (both measured at pH 7) of at least 0.1 PHLU/LU, e.g. at least 0.5, particularly at least 2.

The variants of the invention may have the ability to hydrolyze intact phospholipid, as demonstrated by the PHLU method. They may have A_1 and/or A_2 activity, so they may be able to hydrolyze one or both fatty acyl groups in the phospholipid.

pH optimum

Many variants of the *Humicola lanuginosa* lipase have an alkaline pH optimum for lipase activity and an acid pH optimum for phospholipase activity (e.g. pH 9-10 for lipase and pH 4-6 for phospholipase). Such variants can be used at acid pH (e.g. in oil degumming, described later), as phospholipases with very low concomitant lipase activity.

However, some variants of the *Humicola lanuginosa* lipase which include the substitution G266D,E have pH optima for both lipase and phospholipase activities around pH 5-6. Such variants may be used at acid pH when both lipase and phospholipase activities are desired, e.g. in baking.

Thermostability

The thermostability of the variant can conveniently be evaluated by means of Differential Scanning Calorimetry (DSC). Depending on exact mutations, the variants of the invention generally have similar or slightly lower thermostability than the parent lipolytic enzyme.

The temperature at the top of the denaturation peak (T_d) of the lipase from *Humicola lanuginosa* when heated at 90 deg/hr at pH 5 is just above 70 °C (=T_d). T_d for the variants of the invention is generally 5-10 degrees lower

Use of variant

Depending on the substrate specificity, variants of the invention can be used, e.g., in filtration improvement, vegetable oil treatment, baking, detergents, or preparation of lysophospholipid.

Improvement of filtration

A variant with lysophospholipase activity can be used to improve the filterability of an aqueous solution or slurry of carbohydrate origin by treating it with the variant. This is particularly applicable to a solution or slurry containing a starch hydrolysate, especially a wheat starch hydrolysate since this tends to be difficult to filter and to give cloudy filtrates. The treatment can be done in analogy with EP 219,269 (CPC International).

Vegetable oil treatment

A variant with phospholipase activity can be used in a process for reducing the content of phospholipid in an edible oil, comprising treating the oil with the variant so as to hydrolyze a major part of the phospholipid, and separating an aqueous phase containing the hydrolyzed phospholipid from the oil. This process is applicable to the purification of any edible oil which contains phospholipid, e.g. vegetable oil such as soy bean oil, rape seed oil and sunflower oil. The treatment may be carried out at acid pH, e.g. pH 3-5. Advantageously, a variant can be selected so as to have a high phospholipase activity and a low lipase activity at low pH, due to different pH optima of the two activities.

The process for oil treatment can be conducted according to principles known in the art, e.g. in analogy with US 5,264,367 (Metallgesellschaft, Röhm); K. Dahlke & H. Buchold, INFORM, 6 (12), 1284-91 (1995); H. Buchold, Fat Sci. Technol., 95 (8), 300-304 (1993); JP-A 2-153997 (Showa Sangyo); or EP 654,527 (Metallgesellschaft, Röhm).

Miscellaneous uses of phospholipase

A variant with phospholipase activity can be used to prepare lysophospholipid (e.g. lyso-lecithin) by treating the corresponding phospholipid with the variant, e.g. as described in EP 870840, JP-A 10-42884, JP-A 4-135456 or JP-A 2-49593. The variant can also be used to make mayonnaise, e.g. as described in EP 628256, EP 398666 or EP 319064.

A variant with phospholipase activity may also be used in the processing of dairy and other food products, e.g. as described in EP 567,662 (Nestlé), EP 426,211 (Unilever), EP 166,284 (Nestlé), JP-A 57-189638 (Yakult) or US 4,119,564 (Unilever).

The variant may be used leather treatment, as described in JP-A 7-177884 (Kao).

Baking

A variant with phospholipase and/or DGDGase activity can be used in the preparation of dough, bread and cakes, e.g. to increase dough stability and dough handling properties, or to improve the elasticity of the bread or cake. Thus, the variant can be used in a process for making bread, comprising adding the variant to the ingredients of a dough, kneading the dough and baking the dough to make the bread. This can be done in analogy with US 4,567,046 (Kyowa Hakko), JP-A 60-78529 (QP Corp.), JP-A 62-111629 (QP Corp.), JP-A 63-258528 (QP Corp.), EP 426211 (Unilever) or WO 99/53769 (Novo Nordisk).

It is particularly advantageous to use the variant together with an anti-staling endo-amylase and optionally also to add a phospholipid, to reduce-staling of the bread and particularly to improve softness of the bread in the first 24 hours after baking. The endo-amylase may be a maltogenic α-amylase (e.g. from *Bacillus sp.*, such as Novamyl® from Novo Nordisk) or a fungal or bacterial α-amylase, e.g. from *Aspergillus* or *Bacillus*, particularly *A. oryzae*, *B. licheniformis* or *B. amyloliquefaciens*.

In baking, the variant may have a low activity on short-chain or medium-chain (C_4-C_8), e.g. corresponding to a SLU/LU ratio above 3. The use of such a variant may avoid or suppress the development of an undesired flavor due to the release of short-chain fatty acids. The variant may have activity on triglycerides and phospholipid as well as DGDG.

Cheese flavor

A variant with activity towards short-chain fatty acyl groups may be used to release free fatty acids (FFA) for flavor development in food products, e.g. in cheese ripening, e.g. as described in M. Hanson, ZFL, 41 (10), 664-666 (1990)).

Lipolytic enzyme variants with increased release of short chain fatty compared to long chain fatty acids from milk fat are useful in cheese production, e.g. for flavor enhancement or shortening of the ripening times for ripened cheeses, like cheddar or parmesan. Another application for such lipolytic enzyme variants is for enzyme modified cheese (EMC) for use as flavoring for various food products including process cheese, dressing and snack.

Release of short chain fatty acids, like butyric acid, is essential for the development of cheese flavor, whereas release of long chain fatty acids, like oleic acid, give rise to off flavors. Lipolytic enzyme variants for cheese applications, including EMC, should have SLU/LU ratio of less than 0.5, e.g. less than 0.25, most preferable less than 0.1

Use in detergent

The variant may be used as a detergent additive, e.g. at a concentration (expressed as pure enzyme protein) of 0.001-10 (e.g. 0.01-1) mg per gram of detergent or 0.001-100 (e.g. 0.01-10) mg per liter of wash liquor.

In detergents, the variant may have a high activity on long-chain triglycerides (C_{16}-C_{20}) to improve the removal of fatty soiling. The variant may have phospholipase activity. The variant may have low activity towards short-chain (C_4-C_8) fatty acids in triglycerides, e.g. corresponding to a SLU/LU ratio above 10. The use of such a variant may avoid or suppress the development of an undesired odor due to the release of short-chain fatty acids.

Variants having both lipase and phospholipase activity at alkaline pH may be used in detergents.

Detergent composition

The detergent composition of the invention may for example be formulated as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations. In a laundry detergent, the variant may be effective for the removal of fatty stains, for whiteness maintenance and for dingy cleanup. A laundry detergent composition may be formulated as described in WO 97/04079, WO 97/07202, WO 97/41212, PCT/DK WO 98/08939 and WO 97/43375.

The detergent composition of the invention may particularly be formulated for hand or machine dishwashing operations. e.g. as described in GB 2,247,025 (Unilever) or WO 99/01531 (Procter & Gamble). In a dishwashing composition, the variant may be effective for removal of greasy/oily stains, for prevention of the staining /discoloration of the dishware and plastic components of the dishwasher by highly colored components and the avoidance of lime soap deposits on the dishware.

The detergent composition of the invention may be in any convenient form, e.g., a bar, a tablet, a powder, a granule, a paste or a liquid. A liquid detergent may be aqueous, typically containing up to 70 % water and 0-30 % organic solvent, or non-aqueous.

The detergent composition comprises one or more surfactants, which may be non-ionic including semi-polar and/or anionic and/or cationic and/or zwitterionic. The surfactants are typically present at a level of from 0.1% to 60% by weight, e.g. 0.5-40 %, such as 1-30 %, typically 1.5-20 %.

When included therein the detergent will usually contain from about 1% to about 40% of an anionic surfactant such as linear alkylbenzenesulfonate, alpha-olefinsulfonate, alkyl sulfate (fatty alcohol sulfate), alcohol ethoxysulfate, secondary alkanesulfonate, alpha-sulfo fatty acid methyl ester, alkyl- or alkenylsuccinic acid or soap.

When included therein the detergent will usually contain from about 0.2% to about 40% of a non-ionic surfactant such as alcohol ethoxylate, nonyl-phenol ethoxylate, alkylpolyglycoside, alkyldimethylamine-oxide, ethoxylated fatty acid monoethanol-amide, fatty acid monoethanolamide, polyhydroxy alkyl fatty acid amide, or N-acyl N-alkyl derivatives of glucosamine ("glucamides").

The invention also provides a detergent additive comprising the variant of the invention. The detergent additive as well as the detergent composition may comprise one or more other enzymes such as a protease, a lipase, a cutinase, an amylase, a carbohydrase, a cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a xylanase, an oxidase, e.g., a laccase, and/or a peroxidase.

In general the properties of the chosen enzyme(s) should be compatible with the selected detergent, (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

Proteases: Suitable proteases include those of animal, vegetable or microbial origin. Microbial origin is preferred. Chemically modified or protein engineered mutants are included. The protease may be a serine protease or a metallo protease, e.g. an alkaline microbial protease or a trypsin-like protease. Examples of alkaline proteases are subtilisins, especially those derived from Bacillus, e.g., subtilisin Novo, subtilisin Carlsberg, subtilisin 309, subtilisin 147 and subtilisin 168 (described in WO 89/06279). Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO 89/06270 and WO 94/25583.

Examples of useful proteases are the variants described in WO 92/19729, WO 98/20115, WO 98/20116, and WO 98/34946, especially the variants with substitutions in one or more of the following positions: 27, 36, 57, 76, 87, 97, 101, 104, 120, 123, 167, 170, 194, 206, 218, 222, 224, 235 and 274.

Specific commercially available protease enzymes include Alcalase ®, Savinase ®, Primase ®, Duralase ®, Esperase ®, and Kannase ® (Novo Nordisk A/S), Maxatase ®, Maxacal ®, Maxapem ®, Properase ®, Purafect ®, Purafect OxP ®, FN2 ™, and FN3 ™ (Genencor International Inc.).

Cellulases: Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Suitable cellulases

include cellulases from the genera *Bacillus, Pseudomonas, Humicola, Fusarium, Thielavia, Acremonium*, e.g. the fungal cellulases produced from *Humicola insolens, Myceliophthora thermophila* and *Fusarium oxysporum* disclosed in US 4,435,307, US 5,648,263, US 5,691,178, US 5,776,757 and WO 89/09259.

Especially suitable cellulases are the alkaline or neutral cellulases having colour care benefits. Examples of such cellulases are cellulases described in EP 0 495 257, EP 0 531 372, WO 96/11262, WO 96/29397, WO 98/08940. Other examples are cellulase variants such as those described in WO 94/07998, EP 0 531 315, US 5,457,046, US 5,686,593, US 5,763,254, WO 95/24471, WO 98/12307 and PCT/DK98/00299.

Commercially available cellulases include Celluzyme ®, and Carezyme ® (Novo Nordisk A/S), Clazinase ®, and Puradax HA ® (Genencor International Inc.), and KAC-500(B)® (Kao Corporation).

Peroxidases/Oxidases: Suitable per-oxidases/oxidases include those of plant, bac-terial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from *Coprinus*, e.g. from *C. cinereus*, and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257.

Commercially available peroxidases include Guardzyme ® (Novo Nordisk A/S).

The detergent enzyme(s) may be included in a detergent composition by adding separate additives containing one or more enzymes, or by adding a combined additive comprising all of these enzymes. A detergent additive of the invention, i.e. a separate additive or a combined additive, can be formulated e.g. as a granulate, a liquid, a slurry, etc. Specific detergent additive formulations are granulates, in particular non-dusting granulates, liquids, in particular stabilized liquids, or slurries.

Non-dusting granulates may be produced, e.g., as disclosed in US 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonyl-phenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for in-stance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lac-

tic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238,216.

The detergent may contain 0-65 % of a detergent builder or complexing agent such as zeolite, diphosphate, tripho-sphate, phosphonate, carbonate, citrate, nitrilotriacetic acid, ethylenediaminetetraacetic acid, diethylenetri-aminepen-taacetic acid, alkyl- or alkenylsuccinic acid, soluble silicates or layered silicates (e.g. SKS-6 from Hoechst).

The detergent may comprise one or more polymers. Examples are carboxymethylcellulose, poly(vinyl-pyrrolidone), poly (ethylene glycol), poly(vinyl alcohol), poly(vinylpyridine-N-oxide), poly(vinylimidazole), polycarboxylates such as polyacrylates, maleic/acrylic acid copolymers and lauryl methacrylate/acrylic acid copolymers.

The detergent may contain a bleaching system which may comprise a H2O2 source such as perborate or percarbonate which may be combined with a peracid-forming bleach activator such as tetraacetylethylenediamine or nonanoyloxybenzenesul-fonate. Alternatively, the bleaching system may comprise peroxyacids of e.g. the amide, imide, or sulfone type.

The enzyme(s) of the detergent composition of the invention may be stabilized using conventional stabilizing agents, e.g., a polyol such as propylene glycol or glycerol, a sugar or sugar alcohol, lactic acid, boric acid, or a boric acid derivative, e.g., an aromatic borate ester, or a phenyl boronic acid derivative such as 4-formylphenyl boronic acid, and the composition may be formulated as described in e.g. WO 92/19709 and WO 92/19708.

The detergent may also contain other conventional detergent ingredients such as e.g. fabric conditioners including clays, foam boosters, suds suppressors, anti-corrosion agents, soil-suspending agents, anti-soil redeposition agents, dyes, bactericides, optical brighteners, hydrotropes, tarnish inhibitors, or perfumes.

It is at present contemplated that in the detergent compositions any enzyme, in particular the variant of the invention, may be added in an amount corresponding to 0.01-100 mg of enzyme protein per liter of wash liquor, e.g. 0.05-5 mg of enzyme protein per liter of wash liquor, in particular 0.1-1 mg of enzyme protein per liter of wash liquor.

The variant of the invention may additionally be incorporated in the detergent formulations disclosed in WO 97/07202 which is hereby incorporated as reference.

Methods for preparing enzyme variants

The enzyme variant of the invention can be prepared by methods known in the art, e.g. as described in WO 97/04079 (Novo Nordisk). The following describes methods for the cloning of enzyme-encoding DNA sequences, followed by methods for generating mutations at specific sites within the enzyme-encoding sequence.

Cloning a DNA sequence encoding a enzyme

The DNA sequence encoding a parent enzyme may be isolated from any cell or microorganism producing the enzyme in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the enzyme to be studied. Then, if the amino acid sequence of the enzyme is known, labeled oligonucleotide probes may be synthesized and used to identify enzyme-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to another known enzyme gene could be used as a probe to identify enzyme-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying enzyme-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming enzyme-negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for enzyme (*i.e.* maltose), thereby allowing clones expressing the enzyme to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, *e.g.* the phosphoroamidite method described S.L. Beaucage and M.H. Caruthers, (1981), Tetrahedron Letters 22, p. 1859-1869, or the method described by Matthes et al., (1984), EMBO J. 3, p. 801-805. In the phosphoroamidite method, oligonucleotides are synthesized, *e.g.* in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al., (1988), Science 239, 1988, pp. 487-491.

Site-directed mutagenesis

Once a enzyme-encoding DNA sequence has been isolated, and desirable sites for mutation identified, muta- tions may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites. In a specific method, a single-stranded gap of DNA, the enzyme-encoding sequence, is created in a vector carrying the enzyme gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al., (1984), Biotechnology 2, p. 646-639. US 4,760,025 discloses the introduction of oligonucleotides encoding multiple mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method, because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method for introducing mutations into enzyme-encoding DNA sequences is described in Nelson and Long, (1989), Analytical Biochemistry 180, p. 147-151. It involves the 3-step generation of a PCR fragment containing the desired mutation introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Further, Sierks. et al., (1989) "Site-directed mutagenesis at the active site Trp120 of *Aspergillus awamori* glucoamylase. Protein Eng., 2, 621-625; Sierks et al., (1990), "Catalytic mechanism of fungal glucoamylase as defined by mutagenesis of Asp176, Glu179 and Glu180 in the enzyme from *Aspergillus awamori*". Protein Eng. vol. 3, 193-198; also describes site-directed mutagenesis in an *Aspergillus* glucoamylase.

Expression of enzyme variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

Expression vector

The recombinant expression vector carrying the DNA sequence encoding a enzyme variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. The vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated. Examples of suitable expression vectors include pMT838.

Promoter

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the DNA sequence encoding a enzyme variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* α-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, the TPI (triose phosphate isomerase) promoter from *S. cerevisiae* (Alber et al. (1982), J. Mol. Appl. Genet 1, p. 419-434, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α-amylase, *A. niger* acid stable α-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

Expression vector

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, *e.g.* as described in WO 91/17243.

The procedures used to ligate the DNA construct of the invention encoding a enzyme variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

Host Cells

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a enzyme variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, *e.g.* by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but may be a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are Gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, *e.g. Saccharomyces cerevisiae*.

The host cell may also be a filamentous fungus *e.g.* a strain belonging to a species of *Aspergillus*, such as *Aspergillus oryzae* or *Aspergillus niger, or* a strain of *Fusarium*, such as a strain of *Fusarium oxysporium, Fusarium graminearum* (in the perfect state named *Gribberella zeae*, previously *Sphaeria zeae, synonym with Gibberella roseum and Gibberella roseum* f. sp. *cerealis)*, or *Fusarium sulphureum (*in the prefect state named *Gibberella puricaris,* synonym with *Fusarium trichothecioides, Fusarium bactridioides, Fusarium sambucium, Fusarium roseum,* and *Fusarium roseum var. graminearum), Fusarium cerealis (*synonym with *Fusarium crokkwellnse), or Fusarium venenatum.*

In a specific embodiment of the invention the host cell is a protease deficient of protease minus strain.

This may for instance be the protease deficient strain *Aspergillus oryzae* JaL 125 having the alkaline protease gene named "alp" deleted. This strain is described in WO 97/35956 (Novo Nordisk).

Filamentous fungi cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known per se. The use of *Aspergillus* as a host micro-organism is described in EP 238 023 (Novo Nordisk A/S), the contents of which are hereby incorporated by reference.

Method of producing the enzyme variant of the invention

The enzyme variant of the invention may be produced by a method comprising cultivating a host cell under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the enzyme variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (*e.g.* as described in catalogues of the American Type Culture Collection).

The enzyme variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Expression of variant in plants

The present invention also relates to a transgenic plant, plant part or plant cell which has been transformed with a DNA sequence encoding the variant of the invention so as to express and produce this enzyme in recoverable quantities. The enzyme may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the recombinant enzyme may be used as such.

The transgenic plant can be dicotyledonous or monocotyledonous, for short a dicot or a monocot. Examples of monocot plants are grasses, such as meadow grass (blue grass, Poa), forage grass such as festuca, lolium, temperate grass, such as Agrostis, and cereals, e.g. wheat, oats, rye, barley, rice, sorghum and maize (corn).

Examples of dicot plants are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous (family Brassicaceae), such as cauliflower, oil seed rape and the closely related model organism Arabidopsis thaliana.

Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers. In the present context, also specific plant tissues, such as chloroplast, apoplast, mitochondria, vacuole, peroxisomes and cytoplasm are considered to be a plant part. Furthermore, any plant cell, whatever the tissue origin, is considered to be a plant part.

Also included within the scope of the invention are the progeny of such plants, plant parts and plant cells.

The transgenic plant or plant cell expressing the variant of the invention may be constructed in accordance with methods known in the art. In short the plant or plant cell is constructed by incorporating one or more expression constructs encoding the variant of the invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

Conveniently, the expression construct is a DNA construct which comprises a gene encoding the variant of the invention in operable association with appropriate regulatory sequences required for expression of the gene in the plant or plant part of choice. Furthermore, the expression construct may comprise a selectable marker useful for identifying host cells into which the expression construct has been integrated and DNA sequences necessary for introduction of the construct into the plant in question (the latter depends on the DNA introduction method to be used).

The choice of regulatory sequences, such as promoter and terminator sequences and optionally signal or transit sequences is determined, eg on the basis of when, where and how the enzyme is desired to be expressed. For instance, the expression of the gene encoding the variant of the invention may be constitutive or in-

ducible, or may be developmental, stage or tissue specific, and the gene product may be targeted to a specific tissue or plant part such as seeds or leaves. Regulatory sequences are eg described by Tague et al, Plant, Phys., 86, 506, 1988.

For constitutive expression the 35S-CaMV promoter may be used (Franck et al., 1980. Cell 21: 285-294). Organ-specific promoters may eg be a promoter from storage sink tissues such as seeds, potato tubers, and fruits (Edwards & Coruzzi, 1990. Annu. Rev. Genet. 24: 275-303), or from metabolic sink tissues such as meristems (Ito et al., 1994. Plant Mol. Biol. 24: 863-878), a seed specific promoter such as the glutelin, prolamin, globulin or albumin promoter from rice (Wu et al., Plant and Cell Physiology Vol. 39, No. 8 pp. 885-889 (1998)), a *Vicia faba* promoter from the legumin B4 and the unknown seed protein gene from *Vicia faba* described by Conrad U. et al, Journal of Plant Physiology Vol. 152, No. 6 pp. 708-711 (1998), a promoter from a seed oil body protein (Chen et al., Plant and cell physiology vol. 39, No. 9 pp. 935-941 (1998), the storage protein napA promoter from Brassica napus, or any other seed specific promoter known in the art, eg as described in WO 91/14772. Furthermore, the promoter may be a leaf specific promoter such as the rbcs promoter from rice or tomato (Kyozuka et al., Plant Physiology Vol. 102, No. 3 pp. 991-1000 (1993), the chlorella virus adenine methyltransferase gene promoter (Mitra, A. and Higgins, DW, Plant Molecular Biology Vol. 26, No. 1 pp. 85-93 (1994), or the aldP gene promoter from rice (Kagaya et al., Molecular and General Genetics Vol. 248, No. 6 pp. 668-674 (1995), or a wound inducible promoter such as the potato pin2 promoter (Xu et al, Plant Molecular Biology Vol. 22, No. 4 pp. 573-588 (1993).

A promoter enhancer element may be used to achieve higher expression of the enzyme in the plant. For instance, the promoter enhancer element may be an intron which is placed between the promoter and the nucleotide sequence encoding the enzyme. For instance, Xu et al. *op cit* disclose the use of the first intron of the rice actin 1 gene to enhance expression.

The selectable marker gene and any other parts of the expression construct may be chosen from those available in the art.

The DNA construct is incorporated into the plant genome according to conventional techniques known in the art, including *Agrobacterium*-mediated transformation, virus-mediated transformation, micro injection, particle bombardment, biolistic transformation, and electroporation (Gasser et al, Science, 244, 1293; Potrykus, Bio/Techn. 8, 535, 1990; Shimamoto et al, Nature, 338, 274, 1989).

Presently, *Agrobacterium tumefaciens* mediated gene transfer is the method of choice for generating transgenic dicots (for review Hooykas & Schilperoort, 1992.

Plant Mol. Biol. 19: 15-38), however it can also be used for transforming monocots, although other transformation methods are generally used for these plants. Presently, the method of choice for generating transgenic monocots is particle bombardment (microscopic gold or tungsten particles coated with the transforming DNA) of embryonic calli or developing embryos (Christou, 1992. Plant J. 2: 275-281; Shimamoto, 1994. Curr. Opin. Biotechnol. 5: 158-162; Vasil et al., 1992. Bio/Technology 10: 667-674). An alternative method for transformation of monocots is based on protoplast transformation as described by Omirulleh S, et al., Plant Molecular biology Vol. 21, No. 3 pp. 415-428 (1993).

Following transformation, the transformants having incorporated the expression construct are selected and regenerated into whole plants according to methods well-known in the art.

MATERIALS AND METHODS

Lipase activity on tributyrin (LU)

A substrate for lipase is prepared by emulsifying tributyrin (glycerin tributyrate) using gum Arabic as emulsifier. The hydrolysis of tributyrin at 30 °C at pH 7 is followed in a pH-stat titration experiment. One unit of lipase activity (1 LU) equals the amount of enzyme capable of releasing 1 µmol butyric acid/min at the standard conditions.

Lipase activity on triolein (SLU)

The lipolytic activity may be determined using olive oil as substrate.

In this SLU method, the lipase activity is measured at 30 C and pH 9 with a stabilized olive oil emulsion (Sigma catalog No. 800-1) as the substrate, in a 5 mM Tris buffer containing 40 mM NaCl and 5 mM calcium chloride. 2.5 ml of the substrate is mixed with 12.5 ml buffer, the pH is adjusted to 9, 0.5 ml of diluted lipase sample is added, and the amount of oleic acid formed is followed by titration with a pH stat.

One SLU is the amount of lipase which liberates 1 mole of titratable oleic acid per minute under these conditions.

Phospholipase activity

The following assay methods were used for qualitative or quantitative determination of phospholipase activity.

Phospholipase activity (PHLU)

Phospholipase activity (PHLU) is measured as the release of free fatty acids from lecithin. 50 µl 4% L-alpha- phosphatidylcholine (plant lecithin from Avanti), 4 % Triton X-100, 5 mM $CaCl_2$ in 50 mM HEPES, pH 7 is added 50 µl enzyme solution diluted to an appropriate concentration in 50 mM HEPES, pH 7. The samples are incubated for 10 min at 30 °C and the reaction stopped at 95 °C for 5 min prior to centrifugation (5 min at 7000 rpm). Free fatty acids are determined using the NEFA C kit from Wako Chemicals GmbH; 25 µl reaction mixture is added 250 µl Reagent A and incubated 10 min at 37 °C. Then 500 µl Reagent B is added and the sample is incubated again, 10 min at 37 °C. The absorption at 550 nm is measured using an HP 8452A diode array spectrophotometer. Samples are run in at least in duplicates. Substrate and enzyme blinds (preheated enzyme samples (10 min at 95 °C) + substrate) are included. Oleic acid is used as a fatty acid standard. 1 PHLU equals the amount of enzyme capable of releasing 1 µmol of free fatty acid/min at these conditions.

Phospholipase activity (LEU)

Lecithin is hydrolyzed under constant pH and temperature, and the phospholipase activity is determined as the rate of titrant (0.1N NaOH) consumption during neutralization of the liberated fatty acid.

The substrate is soy lecithin (L-α-Phosphotidyl-Choline), and the conditions are pH 8.00, 40.0°C, reaction time 2 min. The unit is defined relative to a standard.

Phospholipase monolayer assay

On a thoroughly purified surface of a buffer solution (either 10 mM Glycin, pH 9.0 or 10 mM NaOAc, pH 5.0; 1 mM CaCl2, 25°C) a monolayer of Di-Decanoyl-Phosphatidyl Choline (DDPC) is spread from a chloroform solution. After relaxation of the monolayer (evaporation of chlorofom) the surface pressure is adjusted to 15 mN/m, corresponding to a mean molecular area of DDPC of approx. 63 $Å^2$/molec. A solution containing approximately 60 µg (micro gram) enzyme is injected through the monolayer into the subphase of the re-action compartment (cylinder with surface area 2230 mm2 and reaction volume 56570 mm3) in the "zero-order trough". Enzymatic activity is manifested through the speed of a mobile barrier compressing the monolayer in order to maintain constant surface pressure as insoluble substrate molecules are hydrolyzed into more water soluble reaction products. Having verified that the aqueous solubility of the reaction products (capric acid and MDPC) are considerably higher than for DDPC the number of DDPC-molecules hydrolyzed per min-

ute by the enzyme is estimated from the mean molecular area (MMA) of DDPC. The results are calculated on basis of average barrier speed over the first 5 minutes of hydrolysis.

The result is considered positive for phospholipase if the barrier moves at more than 2 mm/min.

Plate assay 1

A) 50 ml 2% agarose in purified water is melted/stirred for 5 minutes and cooled to 60 - 63°C.

B) 50 ml 2% plant L-alpha-Phosphatidylcholine 95% in 0,2M NaOAc, 10 mM $CaCl_2$, pH 5,5 at 60°C in 30 min. is blended in 15 sec. with ultrathorax.

Equal volumes of 2% agarose and 2% Lecithin (A and B) are mixed, and an equal volume of 1 % Triton X-100 is added to this mixture. 250 µl 4 mg/ml crystal violet in purified water is added as indicator. The mixture is poured into appropriate petri dishes (e.g. 30 ml in 14cm Ø dish), and appropriate holes are made in the agar (3-5 mm) for application of enzyme solution.

The enzyme sample is diluted to a concentration corresponding to OD_{280} = 0.5 and 10 microliter is applied into holes in the agarose/lecithin-matrix. Plates are incubated at 30°C and reaction zones in the plates are identified after approx. 4-5 hours and/or after approx. 20 hours incubation. The *Humicola lanuginosa* lipase is used as a control, and the presence of a larger clearing zone than the control is taken as a positive result for phospholipase activity.

In a variation of this assay, the addition of Triton X-100 is omitted.

Plate assay 2

10 g agarose is melted in 550 ml H2O by boiling in a microwave oven. After cooling to 60-70°C the following ingredients are added:

250 ml of a 0.4 M Citrate buffer (pH 4.5 or pH 7.1)

200 ml 3% lecithin (from Avanti) in 2% Triton-X 100

2 ml 2% crystal violet

30 ml of the mixture is poured into 14 cm Ø petri dishes.

The plates are incubated after application of enzyme samples, and the results are interpreted as for Plate assay 1.

Digalactosyl diglyceride hydrolyzing (DGDGase) activity

Monolayer assay 1

On a thoroughly purified surface of a buffer solution (10 mM NaOAc, pH 5.5; 1 mM CaCl2, 25°C; 10 mM beta-cyclodextrin (Sigma C-4767)) a monolayer of DGDG (Sigma (D4651)) is spread from a chloroform solution. After relaxation of the monolayer (evaporation of chlorofom) the surface pressure is adjusted to 15 mN/m. A solution containing approximately 60 µg (micro gram) enzyme is injected through the monolayer into the subphase of the re-action compartment (cylinder with surface area 2230 mm^2 and reaction volume 56570 mm^3) in the "zero-order trough". Enzymatic activity is manifested through increased speed of a mobile barrier compressing the monolayer in order to maintain constant surface pressure as insoluble substrate molecules are hydrolyzed into more water soluble reaction products (in presence of beta cyclodextrin).

The result is considered positive for DGDGase if the barrier moves at more than 1 mm/min.

Monolayer 2

On a thoroughly purified surface of a buffer solution (approx. 75 ml, 10 mM NaOAc, pH 5.5; 1 mM CaCl2, 25°C; 10 mM beta-cyclodextrin (Sigma C-4767)) a monolayer of DGDG (Sigma (D4651)) is spread from a chloroform solution to a surface pressure of about 30 mN/m. After relaxation of the monolayer (evaporation of chlorofom) a solution containing approximately 30 µg (micro gram) purified enzyme is injected through the monolayer into the 75 ml subphase while surface pressure is measured continuously. Enzymatic activity is manifested through increased rate of decrease in surface pressure as DGDG is hydrolyzed into water soluble reaction products (in presence of beta cyclodextrin).

The result is considered positive for DGDGase if maximal drop in surface pressure ($d\pi/dt$) after addition of enzyme exceeds -0.5 mN/min. A number of variants of Lipolase were tested and found to have DGDGase activity, whereas the parent enzyme (Lipolase) only had very limited activity ($d\pi/dt > -0.5$ mN/min.) .

Yeast Strain

Saccharomyces cerevisiae YNG318: MATa leu2-D2 ura3-52 his4-539 pep4-D1[cir+], described in WO 97/04079 and WO 97/07205.

Transformation of yeast strain

The DNA fragments and the opened vectors are mixed and transformed into the yeast *Sac- charomyces cerevisiae* YNG318 by standard methods.

Vector for yeast transformation

pJSO026 (*S. cerevisiae* expression plasmid) is described in WO 97/07205 and in J.S.Okkels, (1996) "A URA3-promoter deletion in a pYES vector increases the expression level of a fungal lipase in Saccharomyces cerevisiae. Recombinant DNA Biotechnology III: The Integration of Biological and Engineering Sciences, vol. 782 of the Annals of the New York Academy of Sciences). It is derived from pYES 2.0 by replacing the inducible GAL1-promoter of pYES 2.0 with the constitutively expressed TPI (triose phosphate isomerase)-promoter from *Saccharomyces cerevisiae* (Albert and Karwasaki, (1982), J. Mol. Appl Genet., 1, 419-434), and deleting a part of the URA3 promoter.

Site-directed mutagenesis

For the construction of variants of a *H. lanuginosa* lipolytic enzyme the commercial kit, Chameleon double-stranded, site-directed mutagenesis kit can be used according to the manufacturer's instructions.

The gene encoding the lipolytic enzyme in question is inserted into the plasmid pHD414. In accord-ance with the manufacturer's instructions the ScaI site of the Ampicillin gene of pHD414 is changed to a MluI site by use of the following primer:

Primer 3: AGAAATCGGGTATCCTTTCAG.

The pHD414 vector comprising the lipolytic gene in question is then used as a template for DNA polymerase and oligos 7258 and 7770.

7258: 5'p gaa tga ctt ggt tga cgc gtc acc agt cac 3'

(Thus changing the ScaI site found in the ampicillin resistance gene and used for cutting to a MluI site).

Primer no. 7770 was used as the selection primer.

7770: 5'p tct agc cca gaa tac tgg atc aaa tc 3' (Changes the ScaI site found in the *H. lanuginosa* lipase gene without changing the amino acid sequence).

The desired mutation (e.g. in the N-terminal of the lipolytic gene or the introduction of a cystein residue) is introduced into the lipolytic gene in question by addition of an appropriate oligos comprising the desired mutation.

PCR reactions are performed according to the manufacturer's recommendations.

Screening method

The yeast libraries are spread on cellulose filters on SC-ura agar plates and incubated for 3-4 days at 30°C.

The filters are then transferred to the lecithin plates and incubated at 37°C for 2-6 hours. Yeast cells harboring active phospholipases will develop white clearing zones around the colonies. The positive variants can then be further purified and tested.

Media

SC-ura medium

Yeast Nitrogen (without amino aicds)	7.5 g
Succinic acid	11.3 g
NaOH	6.8 g
Casaminoacid (without vitamins)	5.6 g
Tryptophan	0.1 g
Agar, Merck	20 g
Distilled water	ad 1000 ml

Autoclaved for 20 minutes at 121°C.

From a sterile stock solution of 5% Threonine 4 ml is added to a volume of 900 ml together with 100 ml of a sterile 20% glucose.

EXAMPLES

Example 1: Construction of variants with the backbone from *Humicola* lanuginosa lipase and C-terminal from *Fusarium oxysporum* phospholipase by PCR reaction

The following variants were used as templates for the backbone from the *Humicola lanuginosa* lipase: E1A +G91A +D96W +E99K +Q249R and SPIRR +G91A +D96W +E99K +Q249R. The parent lipase was used for generating a fragment in the C-terminal without Q249R. The template for the C-terminal phospholipase was the *Fusarium oxysporum* phospholipase, cloned in the same vector as the variants of *Humicola lanuginosa* lipase.

PCR reaction 1: 4244 (SEQ ID NO: 1) as 5' primer and H7 (SEQ ID NO: 6) as 3'primer and one of the two templates mentioned above.

PCR reaction 2: FOL14 (SEQ ID NO: 3) as 5' primer and FOL15 (SEQ ID NO: 4) as 3' primer and *Humicola lanuginosa* lipase as template (no mutation in pos 249)

PCR reaction 3: FOL16 (SEQ ID NO: 5) as 5' primer and AP (SEQ ID NO: 2) as 3' primer and F.o. phospholipase as template

A PCR reaction 4 was made to create the connection between the *Humicola lanuginosa* lipase variant and the C-terminal from the phospholipase by using FOL14

(SEQ ID NO: 3) as 5' primer and AP (SEQ ID NO: 2) as 3' primer and PCR reaction 2 and 3 as template.

The final PCR was made with 4244 (SEQ ID NO: 1) as 5' primer and KBoj14 (SEQ ID NO: 7) as 3' primer and PCR re-action 1 and 4 as template (by using *Humicola lanuginosa* lipase as template in reaction 2 a possibility to omit the mutation in position 249 was created).

The final PCR fragment was used in an in vivo recombination in yeast together with pJSO026 cut with the restriction enzymes. SmaI(or BamHI) and XbaI (to remove the coding region and at the same time create an overlap of about 75 bp in each end to make a recombination event possible). This final treatment was also used in the following examples.

Primer FOL14 (SEQ ID NO: 3) and primer 15/16 are mixed oligoes to give the possibility to bind both with *Humicola lanuginosa* lipase and phospholipase templates and at the same time give possibilities for introducing the amino acids from both templates in the different positions. For some of the positions new amino acids could be introduced as well.

Primer FOL14 (SEQ ID NO: 3)

Position 205 in the *H. lanuginosa* lipase: 75% R, 25% S

Primer FOL15 (SEQ ID NO: 4) /FOL16 (SEQ ID NO: 5)

Position 256 in the *H. lanuginosa* lipase: 50% P, 50% A

Position 260 in the *H. lanuginosa* lipase: 25% R, 12.5% Q, 12.5% H, 12.5% C, 12.5% Y, 12.5% W, 12.5% stop.

The sequences of the resulting variants were determined, and were found to correspond to *Humicola lanuginosa* lipase with the following alterations. Alterations in parentheses are uncertain.

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

E1A, G91A, D96W, E99K, E239C, Q249R, P256A, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G273F, (274S)

E1A, G91A, D96W, E99K, N248T, Q249R, W260Q, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

SPIRR, G91A, D96W, E99K, W260C, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272, G273F, (274S)

SPIRR, G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

E1A, G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Example 2: Production of truncated sequences

Variants were made with stop after amino acid 269, 270, 271, 272,(273 and 274)

The following PCR reactions were made with the following template: E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S).

Reaction 1: 5' primer 4244 (SEQ ID NO: 1) and 3' primer KBoj36 (stop after 269)

Reaction 2: 5' primer 4244 (SEQ ID NO: 1) and 3' primer KBoj37 (stop after 270)

Reaction 3: 5' primer 4244 (SEQ ID NO: 1) and 3' primer KBoj38 (stop after 271)

Reaction 4: 5' primer 4244 (SEQ ID NO: 1) and 3' primer KBoj39 (stop after 272)

The sequences of the resulting variants were determined, and were found to correspond to *Humicola lanuginosa* lipase with the following alterations:

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G

Example 3: Removal of mutations in the lid region

G91A or E99K can be removed without loosing the phospholipase activity. The sequences of the resulting variants were determined, and were found to correspond to *Humicola lanuginosa* lipase with the following alterations:

E1A, G91A, D96W, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

SPIRR, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

SPIRR, G91A, D96W, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

E1A, G91A, D96W, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)

Example 4: Doping in the C-terminal region of Humicola lanuginosa lipase to introduce phospholipase activity

Three different libraries were constructed with possibilities for mutations in position 256 and position 263-269. At the same time possibilities for extension of the C-terminal with either 1, 2 , 3 or 4 amino acids were included.

Doping, the wt sequences are underlined:

256: P 94, A 3, T 3

263: G 87, E 4.8, A 3.8, R 3.6, Q 0.2, P 0.2

264: L 87, P 4.8, Q 3.8, V 3.6, A 0.2, E 0.2

265: I 85, T 5.6, L 2.2, S 1.6, N 1.5, F 1.4, R 0.4, K 0.4 A,P 0.1, G,D,C,H,Y 0.03, Q,E 0.01, stop 0.016

266: G 86, D 5.9, R 2, S 1.7, C 1.6, A 0.9, V 0.9, E 0.7, W 0.2, H,Y 0.1, I,L,T,F,P 0.02, Q,K 0.01, stop 0.014

267: T 86, A 6.6, S 1.9, R 0.9, N 0.9, I 0.9, K 0.9, M 0.9, P 0.9, P 0.9, G,V 0.14, D,E 0.07, L 0.03, C,Q,H,F,W,Y 0.01, stop 0.01

268: C 91, S 1.9, R 1.0, G 1.0, F 0.9, Y 0.9, L 0.04, A,N,D,H,I,P,T,V 0.01, stop 2.8

269: L 92, stop 8 (KBoj 32 (SEQ ID NO: 8) and KBoj33)/ N 86, K 2.7, D 1.8, H 1.8, I 1.8, S 1.8, T 1.9, Y 1.8, R 0.1, Q,M,E 0.06, A,C,G,L,F,P,V 0.04, stop 0.06(KBoj34)

270: stop 100 (KBoj33)/A 44, P 44, S 1.9, T 1.8, R 1.5, L 1.5, G 1.4, V 1.4, D 0.7, Q 0.7, E 0.7, H 0.7, N,C,I,K,M,F,W,Y 0.03, stop 0.03 (KBoj 32 (SEQ ID NO: 8) and KBoj 34)

271: G 72, R 4.5, V 3.2, E 3.0, C 2.9, A 1.6, S 1.2, D 1.0, L 0.5, I,K,Y 0.15, Q,T 0.08, N,P 0.05, stop 9.2

272: G 72, R 4.5, V 3.2, E 3.0, C 2.9, A 1.6, S 1.2, D 1.0, L 0.5, I,K,Y 0.15, Q,T 0.08, N,P 0.05, stop 9.2

273: F 74, L 11, S 2.8, I 2.7, V 2.7, Y 2.5, C 2.5, A,R,T 0.1, N,D,H 0.08, Q,E,K 0.01, stop 0.5

274 STOP

Library A: PCR reaction with 4244 (SEQ ID NO: 1) as 5' primer and KBoj 33 as 3' primer and E1A +G91A +D96W +E99K +Q249R or E1A +G225R as template. Variants from this library will be without extension.

Library B: PCR reaction with 4244 (SEQ ID NO: 1) as 5' primer and KBoj 32 (SEQ ID NO: 8) as 3' primer and E1A +G91A +D96W +E99K +Q249R or E1A +G225R as template. Variants from this library will most probably contain a C-terminal extension but can contain stop codons before the extension.

Library C: PCR reaction with 4244 (SEQ ID NO: 1) as 5' primer and KBoj 34 as 3' primer and E1A +G91A +D96W +E99K +Q249R or E1A +G225R as template. Variants from this library will most probably contain mutations in position 269 and a C-terminal extension but can contain stop codons before the extension.

The following variants were obtained:

Library A:

E1A +G91A +D96W +E99K +Q249R +G266D

Library B:

E1A +G91A +D96W +E99K +(R232L) +Q249R +G266S +270A
E1A +G91A +D96W +E99K +Q249R +G266S +270D +271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264G+ I265G+ G266F+ T267stop
E1A +G91A +D96W +E99K +Q249R +G266A +270P +271G
E1A +G91A +D96W +E99K +Q249R +L264P +I265F +L269stop

Library C:

E1A +G91A +D96W +E99K +Q249R +G263E +G266D +L269N +270P +271V +272G +273F
E1A +G91A +D96W +E99K +Q249R +G263A +G266S +L269N +270A +271G +272R +273F
E1A +G91A +D96W +E99K +Q249R +L264P -G266 +L269I +270P +271R +272G +273F
E1A +G91A +D96W +E99K +Q249R +G266D +L269S +270A +271G +272G +273F
E1A +D27G +G91A +D96W +E99K +Q249R +G266S +L269N +270A +271G +272G +273F
E1A +G91A +D96W +E99K +Q249R +G266D +L269N +270A
E1A +G91A +D96W +E99K +Q249R +L264P +L267Q +L269N
E1A +G91A +D96W +E99K +Q249R +G263R +I265L +L269N +270P

Example 5: For some of the above variants, the pH optimum for lipase and phospholipase was determined by using the LU and PHLU methods at various pH values. The results showed that the pH optimum phospholipase activity was in the range 4-6. The optimum for lipase activity varied from about pH 6 to about pH 10.

8 variants listed in Example 5 were analyzed for phospholipase activity by the mono layer assay described above at pH 5 and 9. The results showed that all the variants have phospholipase activity at pH 5 and 9, whereas the parent lipase

(*Humicola lanuginosa* lipase) showed no activity at pH 5 or 9. Depending on the variant, the activity at pH 5 was higher or lower than at pH 9.

A prior-art variant of *Humicola lanuginosa* lipase was found to have no phospholipase activity at pH 5: SPIRR +N94K +F95L +D96H +N101S +F181L +D234Y +I252L +P256T +G263A +L264Q.

Example 5: Variants of *Humicola* lipase with phospholipase activity

Variants of the parent lipase from *Humicola lanuginosa* were prepared and tested for phospholipase activity as described above. The following variants were found to have phospholipase activity, where as the parent had no phospholipase activity by the same method.

E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
SPIRR, G91A, D96W, E99K, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
E1A, G91A, D96W, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N, 270A, 271G, 272G, 273F, (274S)
E1A, G91A, D96W, E99K, P256A, W260H, G263Q, L264A, I265T, G266D, T267A, L269N
E1A, G91A, D96W, E99K, Q249R, G266S, 270D, 271G
E1A, G91A, D96W, E99K, Q249R, G266D
E1A, G91A, D96W, E99K, Q249R, G266A, 270P, 271G
G266D
E1SPPCGRRP +E99N +E239C +Q249R +G266D
E1SPPCGRRP +E239C +Q249R +G266D
E1SPPCGRRP +L93K +E99K +E239C +Q249R +G266D
E1SPPCGRRP +E99K +E239C +Q249R +G266D
G266A
G266W
G266V
G263Q +L264A +I265T +G266D +T267A
G263F +L264A +G266S +T267E
E1SPPCGRRP +E239C +Q249R +G263Q +L264A +I265T +G266D +T267A
G266S

G266L
G263A +G266A
G263A +G266Y
E1SPPCGRRP +E239C +Q249R +G266A
E1SPPCGRRP +E239C +Q249R +G266S
E1SPPCGRRP +E239C +Q249R +G263F +L264A +G266S +T267E
D62A + G266A
D62A + G266S
D96S + G266A
D96S+ G266S
D96S+ G266R
D96S+ G266W
D96S+ G266V
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ L264P+ G266S
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPCGRRP + G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop
G263D +L264I +I265N +G266E +T267GS
E219G +L264I +I265N +G266T +T267GL
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ E239C+ Q249R+ P256A+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G +273F (+274S)
E1A+ G91A+ D96W+ E99K+ N248T+ Q249R+ W260Q+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR+ G91A+ D96W+ E99K+ W260C+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272+ G273F (+274S)
SPIRR+ G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+

270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G +272G +273F (+274S)
SPIRR+ D96W+ E99K+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
SPIRR+ G91A+ D96W+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N
E1A+ G91A+ D96W+ E99K+ Q249R+ G263E+ G266D+ L269N+ 270P+ 271V+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G263A+ G266S+ L269N+ 270A+ 271G+ 272R+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ Δ266+ L269I+ 270P+ 271R+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264C+ I265N+ G266P+ T267stop
E1A+ G91A+ D96W+ E99K (+R232L)+ Q249R+ G266S+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ 270D+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264F+ Δ266+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264G+ I265G+ G266F+ T267stop
E1A+ G91A+ D96W+ E99K+ Q249R+ L264stop
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G
E1A+ G91A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A+ 270P+ 271G
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ I265F+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269S+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ G266D+ L269N+ 270A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ L269N+ 270A+ 271G+ 272G+ 273F
E1A+ G91A+ D96W+ E99K+ Q249R+ L264P+ L267Q+ L269N

E1A+ G91A+ D96W+ E99K+ Q249R+ G263R+ I265L+ L269N+ 270P
E1A+ D96W+ E99K+ P256A+ W260H+ G263Q+ L264A+ I265T+ G266D+ T267A+ L269N+ 270A+ 271G+ 272G+ 273F (+274S)
E1A+ G225R+ G266D
E1A+ G225R+ G263A+ I265V+ G266S
E1A+ G225R+ G263A+ T267A
E1SPPCGRRP+ D96S+ E239C+ Q249R+ I252M+ L264Q+ G266D
E1SPPCGRRP+ G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPCGRRP+ D96S+ E239C+ Q249R+ G266D
E1SPPCGRRP+ D96S+ E239C+ Q249R+ G266C+ L267A
E1A+ G91A+ D96W+ E99K+ Q249R+ G266A
E1A+ D96M+ G106S+ G225R+ G266D
E1A+ D96Q+ G106S+ G225R+ G266S
E1A+ D96F+ G225R+ G266S
E1A+ D96C+ G225R+ G266T
E1A+ D96H+ G106S+ G225R+ G266S
SPIRR+ D96S+ G266D
SPIRR+ D96R+ G106S+ G266D
SPIRR+ D96I+ G106S+ G266S
SPIRR+ D96W+ K237R+ G266S
SPIRR+ G266A
SPIRR+ D96S+ G106S+ G225R+ G266D
SPIRR+ D96Q+ G106S+ G225R+ G266A
SPIRR+ D96Y+ G106S+ G225R+ G266N
SPIRR+ D96C+ G106S+ G225R+ G266T
SPIRR+ D96H+ T186I+ G225R+ G266S
E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ G266S
E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ G263E+ G266S+ 270A
E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ L264P+ G266S

E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ P256T+ G266D
E1SPPRRP+ G91A+ D96W+ E239C+ Q249R+ G266C+ T267P+ L269stop
E1A+ G91A+ D96W+ E99K+ Q249R+ G266S+ T267S
E1SPPCGRRP+ G91A+ D96W+ E239C+ Q249R+ P256T+ G266S
E1SPPCGRRP+ E239C+ Q249R+ P256T+ G266S+ T267A
E1SPPCGRRP+ E239C+ Q249R+ G266D
E1SPPCGRRP+ G91A+ D96W+ E239C+ Q249R+ G266D
E1SPPRRP+ D96S+ E239C+ Q249R+ G266D
L259S
G266D
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
G266E
G263A +G266A
E1SPCRPRP +E239C +Q249R +G266A
E1SPCRPRP +E239C +Q249R +G266S
D96S + G266A
D96S + G266S
D96S + G266W
E1SPPCGRRP +D96S +E239C +Q249R +G263D +L264I +I265N +G266E +T267GS
E1SPPCGRRP +D96S +E239C +Q249R +L264I +I265N +G266T +T267GL
D96F +G266A
D96F +G266S
E1SPPCGRRP +E99N +E239C +Q249R +G266A
E1SPPCGRRP + D96S +E239C +Q249R +G266A
E1SPPCGRRP + D96S +E239C +Q249R +G266S
E1SPPCGRRP + D96S +E239C +Q249R +G263F +L264A +G266S +T267E
V60G +D62A +S83T +R84K +D96W +G266D
V60G +D62A +S83T +D96W +G266D
V60G +D62A +S83T +D96W +G266W

L259I
L259N
D96W +G263Q +L264A +I265T +G266D +T267A

In the table above, (+274S) indicates that the presence of this amino acid residue at the C-terminal is uncertain. For one such variant, it was found that only a minor fraction contained this residue

Several of the above variants had a higher ratio of phospholipase (PHLU) to lipase (LU) than a prior-art enzyme from *F. oxysporum* known to have both lipase and phospholipase activity.

For some of the above variants, the pH optimum for lipase and phospholipase was determined by using the LU and PHLU methods at various pH values. The results showed that the pH optimum phospholipase activity was in the range 4-6. The optimum for lipase activity varied from about pH 6 to about pH 10.

8 variants listed in Example 5 were analyzed for phospholipase activity by the mono layer assay described above at pH 5 and 9. The results showed that all the variants have phospholipase activity at pH 5 and 9, whereas the parent lipase (*Humicola lanuginosa* lipase) showed no activity at pH 5 or 9. Depending on the variant, the activity at pH 5 was higher or lower than at pH 9.

A prior-art variant of *Humicola lanuginosa* lipase was found to have no phospholipase activity at pH 5: SPIRR +N94K +F95L +D96H +N101S +F181L +D234Y +I252L +P256T +G263A +L264Q.

The following variants of the parent lipase from *Humicola lanuginosa* may also have phospholipase activity:

D62A +S83T +D96W +G266S
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96L +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96N +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96A +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96E +E99K +G263Q +L264A +I265T +G266D +T267A +L269N

+270A +271G +272G +273F +274S
G91A +D96S +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96R +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96G +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96Q +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S +
R84W +G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S +
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96W +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96W +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S

Example 6: Variants of *Rhizomucor* lipase with phospholipase activity

The following two variants of the parent lipase from *Rhizomucor miehei* were prepared and tested for phospholipase activity as described above. The variants were found to have phospholipase activity, where as the parent had no phospholipase activity by the same method.

G266N

G266V

Example 7: Variants of *Humicola* lipase with increased specificity for long-chain fatty acids

Variants of the parent lipase from *Humicola lanuginosa* were prepared and tested for their hydrolytic activity on two triglyceride substrates with different chain length: tributyrin ($C_{4:0}$) and triolein ($C_{18:1}$). The tests were done at pH 9 by the LU and SLU methods described above. The following variants were found to have a higher ratio of triolein activity to tributyrin activity than the parent enzyme (*Humicola lanuginosa* lipase):

E1SPIRPRP +G91A +D96N +E99K +Q249R
E1SPCRPRP+ S83T+ N94K+ D96L+ E239C+ Q249R
G266D
E1SPIRPRP +D62A +E99K +Q249R
E1SPIRPRP +D62G +E99K +Q249R
E1SPIRPRP +D62V +E99K +Q249R
E1SPIRPRP +R84W +E99K +Q249R
E1SPIRPRP +R84K +E99K +Q249R
E1SPIRPRP + K98D +E99K +Q249R
E1SPIRPRP + E99K +Q249R + 270PGLPFKRV
E1SPPCGRRP + E99N +N101S +T231K +R232G +D234G +E239C +Q249R
E1SPIRPRP +E99K +Q249R + 270PWPARLGRL
L93K +D96G
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A+ 271G+ 272G+ 273F (+274S)
E1SPCRPRP +V60G +E99N +S119G +R209P +E239C +Q249R
G266A
G266E
G266V
G263Q +L264A +I265T +G266D +T267A
G266L
G263A +G266A
E1SPCRPRP +E239C +Q249R +G266A

E1SPCRPRP +E239C +Q249R +G266S
D96S + G266A
D96S + G266S
D96S + G266W
L264I +I265N +G266T +T267GL
E1SPPCGRRP +D96S +E239C +Q249R +L264I +I265N +G266T +T267GL
D96F +G266A
D96F +G266S
E1SPPCGRRP +E99N +E239C +Q249R +G266A
E1SPPCGRRP + D96S +E239C +Q249R +G266A
E1SPPCGRRP + D96S +E239C +Q249R +G266S
D62A + S83T
E1SPPCGRRP +K98D +E99N +E239C +Q249R
T231R +N233R +270CP
E1SPPCGRRP +E99N +E239C +Q249R +270MD
E1SPPCGRRP + D62A +S83T +E99N +E239C +Q249R
D62A +S83T + G91A +E99K +T231R +N233R +Q249R
V60G +D62A +S83T +R84K +D96W +G266D
L259N
L259R
L259M
L259Q
SPPCGRRP(-E) +R84W +E99N +N101S +E239C +Q249R
R84W +G91A +E99K +T231R +N233R +Q249R
Y21I
Y21V
SPIRPRP(-E) +R84L +E99K +Q249R
Y21C
SPIRPRP(-E) +D62 +E99K +Q249R
D96W +G263Q +L264A +I265T +G266D +T267A +L269N +A270 +G271 +G272 +F273

+S274.
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S

The following variants of the parent lipase from *Humicola lanuginosa* may also have an increased specificity for long-chain fatty acids:

SPIRPRP(-E) +V60R +D62V +L93K +E99K +Q249R
SPIRPRP(-E) +D62V +E99K +Q249R
SPIRPRP(-E) +E99K +Q249R +P256D
SPIRPRP(-E) +D62V +E99K +Q249R +P256D
SPIRPRP(-E) +D62V +E99K +Q249R +P256S
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96L +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96N +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96A +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96E +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96S +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96R +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96G +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96Q +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96W +E99K +G263Q +L264A +I265T +G266S +T267A +L269N

+270A +271G +272G +273F +274S
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266S +T267A +L269N +270A +271G +272G +273F +274S
R84W +G91A +D96F +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270A +271G +272G +273F +274S
SPPCGRRP(-E) +V60G +D62E +S83T +R84K +E99N +N101S +E239C +Q249R
V60G +D62E +S83T +R84K +G91A +E99K +T231R +N233R +Q249R

Example 8: Variants of *Fusarium* lipase with increased specificity for long-chain fatty acids

Variants of the parent lipase from *Fusarium oxysporum* were prepared and tested as in the previous example. The following variants were found to have a higher ratio of triolein activity to tributyrin activity than the parent enzyme:

Y23S

Y260L

The following variants of the parent lipase from *Fusarium oxysporum* may also have an increased specificity for long-chain fatty acids:

R80H +S82T

S82T +A129T

Example 9: Variants of *Rhizomucor* lipase with increased specificity for long-chain fatty acids

The following variants of the parent lipase from *Rhizomucor miehei* may have an increased specificity for long-chain fatty acids:

Y260W

Y28L

Y28C +H217N

Example 10: Variants of *Humicola* lipase with increased specificity for short-chain fatty acids

Variants of the parent lipase from *Humicola lanuginosa* were prepared and tested as in the previous example. The following variants were found to have a higher ratio of tributyrin activity to triolein activity (a lower SLU/LU ratio) than the parent enzyme:

SPIRPRP(-E) +E99K +R195Q +R209E +Q249R
N101R +R195Q +R209E +L259S +Y261D
N101R +R195Q +R209E +L259S
N101R +L259S +Y261D
N101R +L259S
Y261D
L259S
SPIRPRP(-E) +E99K +N101R +Q249R
G263D +L264I +I265N +G266E +T267GS
Y261I
D234R
Y261K

The following variants of the parent lipase from *Humicola lanuginosa* may also have a higher ratio of tributyrin activity to triolein activity:

N101R,R195Q,R209E,L259S,Y261D
N101R,R195Q,R209E,L259S
N101R,L259S,Y261D
N101R,L259S

Example 11: Variants of *Fusarium* lipase with increased specificity for short-chain fatty acids

Variants of the parent lipase from *Fusarium oxysporum* were prepared and tested as in the previous example. The following variants were found to have a higher ratio of tributyrin activity to triolein activity than the parent enzyme:

Y23W
Y260D
Y260R
Y260C
Y260N

Example 12: Variants of *Rhizomucor* lipase with increased specificity for short-chain fatty acids

The following variants of the parent lipase from *Rhizomucor miehei* may have an increased specificity for short-chain fatty acids:

Y260C
Y260G
Y260V

Example 13: Variants of *Humicola* lipase with DGDGase activity

Variants of the parent lipase from *Humicola lanuginosa* were prepared, and the hydrolytic activity towards DGDG (di-galactosyl-di-glyceride) was determined as described above. The following variants were found to have DGDGase activity, whereas the parent lipase gave a negative result.

D96W +G263Q +L264A +I265T +G266D +T267A
G263Q +L264A +I265T +G266D +T267A
D96W +G263Q +L264A +I265T +G266D +T267A +L269N +270AGGFS
G91A +D96W +E99K +G263Q +L264A +I265T +G266D +T267A +L269N +270AGGFS
D96F +G266S

Example 14: Variants of *Humicola* lipase with increased pH optimum

Variants of the parent lipase from *Humicola lanuginosa* were prepared, and the lipase activity was measured by the LU method at pH 7 and 9. The following variants were found to have a higher ratio of activity at pH 9 to activity at pH 7 than the parent lipase:

R84L
R84W
Y21I
Y21V
Y261I

Example 15: Variants of *Humicola* lipase with decreased pH optimum

Variants of the parent lipase from *Humicola lanuginosa* were prepared, and the lipase activity was measured by the LU method at pH 7 and 9. The following variants were found to have a lower ratio of activity at pH 9 to activity at pH 7 than the parent lipase:

Y261D
G266D/E
Y261W

Example 16: Use of *Humicola* lipase variants in degumming of vegetable oil

Rapeseed oil was treated with two variants of the lipase from *Humicola lanuginosa*, essentially as described in Example 6 of WO 98/18912 (Novo Nordisk).

One variant was tested at an enzyme dosage of 0.6 mg of enzyme protein per kg of oil. Results of tests at various pH and temperatures showed optimum performance at pH 5.7, 35-45°C, where a final P content of 4 ppm was reached. A separate experiment at 45°C, pH 6 showed that a final P content of 4 ppm could be reached at an enzyme dosage as low as 0.15 mg/kg.

A similar experiment with another *Humicola lanuginosa* lipase variant showed optimum performance at 40°C, pH 5.0-5.5. The enzyme dosage was 0.3 mg/kg.

A degumming experiment was made with a third *Humicola lanuginosa* lipase variant, using rape seed oil at 45°C, pH 5, 1.8 mg enzyme/kg oil. For comparison, a similar experiment was made with the parent lipase (*Humicola lanuginosa* lipase) at 18 mg/kg. The results showed that good degumming (<10 ppm residual P content) was obtained in 3.4 hours with the variant.

The parent lipase (*Humicola lanuginosa* lipase) was found to have very little degumming effect, even at 10 times higher enzyme dosage.

Example 17: Use of lipase variants in baking

A variant of the lipase from *Humicola lanuginosa* was evaluated in baking tests as follows.

Doughs were prepared from Meneba flour according to the European straight dough method (ABF-SP-1201.01) with 40 ppm of ascorbic acid. Various combinations of additives at the following dosages were used: the lipase variant at 0, 0.25, 0.5 or 1.5 mg/kg; phospholipid (lecithin) at 0 or 10 g/kg; and endo-amylase at 0 or 750 MANU/kg.

The endo-amylase was maltogenic amylase from *B. stearothermophilus* (tradename Novamyl ®). One MANU (Maltogenic Amylase Novo Unit) is defined as the amount of enzyme required to release one μmol of maltose per minute at a concentration of 10 mg of maltotriose substrate per ml of 0.1 M citrate buffer, pH 5.0 at 37°C for 30 minutes.

After baking, the loaves were cooled, and the loaf volume, crumb firmness and softness were evaluated after approximately 2 hours. The evaluation was repeated after 1, 3 and 7 days storage at 22°C wrapped in double plastic bags.

Firmness of crumb was measured using a texture analyzer TA-XT2 from Stable Micro Systems (probe diameter 40 mm).

Softness in gram was measured as the force needed to press a probe 6.25 mm into a crumb of a 25 mm thick slice of bread (25 % penetration).

The results showed that the addition of 1.5 mg of the variant increased the loaf volume. The results for firmness and elasticity show that the variant gives significantly softer crumb and significantly better elasticity from day 0 to day 7.

Example 18: Use of lipase variants for dough stability in baking

A variant of the *Humicola lanuginosa* lipase was evaluated in a baking trial to evaluate its tolerance towards extended proofing of the dough.

Doughs were prepared from Pelikan flour according to the European straight dough method (347-SP-1217) with 30 ppm ascorbic acid, fungal α-amylase (10 FAU of Fungamyl), and pentosanase (100 FXU of Pentopan Mono). Dosages of 0.2, 0.4, and 0.6 mg enzyme protein/kg flour of the variant were compared with 1000 LU of the parent lipase.

The doughs were made into rolls. Half of the rolls were proofed for 45 minutes (normal proofing) and the other half for 70 minutes (over proofing).

After baking the bread was cooled, and the volume and the standing of the rolls were evaluated after approximately 2 hours. The standing is a measure of the shape of the rolls and is defined as the height of 10 rolls divided by the width of 10 rolls, which means that nice round loaves have a high standing value, whereas flat rolls have a low standing value.

The results showed that at normal proofing time the volume of 0.4 and 0.6 mg of the variant were better than that of the parent lipase, and the standing of the rolls were better for the variant at all dosages than for the parent lipase. When the rolls were over proofed, both volume and standing was better for the variant at all dosages than for the parent lipase.

Example 19: Effect of lipase variants on off-odor development

The development of off-odor from lipases with different chain-length specificity was evaluated in whole milk. The developed butyric acid/sour odor was evaluated by sniffing the samples after heating.

25 ml whole milk was placed in 100 ml blue cap flasks (with caps) in a 32°C water bath. Of each of the lipases listed below, 0.2 mg enzyme protein per litre milk was added to the flasks. The temperature was raised to 45°C, and evaluation took place after 15 and 105 minutes.

The lipases tested were *Humicola lanuginosa* lipase and variants thereof. For each lipase, the chain-length specificity is expressed as the ratio of activities on triolein (SLU) and tributyrin (LU).

Three persons evaluated the samples and agreed on the ranking shown below

+ Detectable smell
++ Clear and characteristic butyric acid and/or sour odor
+++ Strong butyric acid and/or sour odor

Three variants of *Humicola lanuginosa* lipase having a higher SLU/LU ratio than *Humicola lanuginosa* lipase were found to have less malodor than the parent lipase.

Example 20: Effect of lipase variants on malodour on textile after washing

Soiling:

Cotton textile was soiled with a dairy product as described here. 50 mg of butter was applied over an area of approximately 30 cm^2 in an even spot. The soiled textile was aged for 24 hours at ambient conditions.

Washing procedure:

Washing of the soiled textile was done in a Terg-O-tometer using a commercial detergent(5 g/l) with and without lipase(1250 and 5000 LU/l). The washing was done at 30°C for 20 min at 100 rpm. After washing the swatches were left overnight to dry at ambient conditions.

Sensory analysis:

Next day, the malodour was assessed by a sensory panel consisting of at least 10 trained assessors. Samples were kept in tight glass jars and left at least 30 minutes between every evaluation for accumulation of malodour. Swatches were taken out and the malodour assessed on the textile. The butyric acid malodour was scored according to the scale below. As a reference the sample washed without lipase was used.

0. Fainter smell than reference
1. Same as reference
2. Slightly stronger than reference
3. Definitely stronger than reference
4. Stronger than 3.

Variants of *Humicola lanuginosa* lipase with an increased ratio of triolein/tributyrin activities (increased SLU/LU ratio) were found to give a fainter smell from butter stains than the parent enzyme (*Humicola lanuginosa* lipase). A separate washing experiment showed that the variants, like the parent enzyme, were effective in the removal of lard stains.

Alternative methods

The intensity of butyric acid from dairy stains on fabric can also be evaluated by instrumental analysis:

1. By Head Space Gas Chromatography, or
2. By extraction of the odours from fabric followed by Gas Chromatography

Example 21: Effect of lipase variants on odour of bread baked with butter

Six variants of the lipase from *Humicola lanuginosa* were prepared and were evaluated in bread baked by the European straight dough procedure (347-SP-1217) with addition of 3% butter. 0.2 mg enzyme protein/kg flour was used for each of the variants.

The chain-length specificity of the variants was also determined by measuring the triolein/tributyrin activity ratio (SLU/LU described above). The parent lipase from *Humicola lanuginosa* and a prior-art lipase with phospholipase acivity from *Fusarium oxysporum* were also tested for comparison.

The results are summarized below:

\+ detectable smell

++ clear and characteristic butyric acid and/or sour odour

+++ strong butyric acid and/or sour odour

	SLU/LU	Rating
Variants of the	2.7	(+)
	3	no effect
	7	no effect

invention	28	no effect
	70	no effect
Parent lipase	1.2	++
Prior-art lipase	1.1	+++
Control (no lipase)	-	no effect

The results indicate that that lipase variants with a SLU/LU ratio at 3 or above (i.e. a high specificity for long-chain fatty acids) give no unpleasant odour in bread baking even with butter in the recipe.

CLAIMS

1. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme having an alcohol binding site having a glycerol part with an sn2 position,

c) in the parent lipolytic enzyme selecting at least one amino acid residue which comprises at least one atom within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride in a three-dimensional structure of the parent lipolytic enzyme and the substrate,

d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

f) preparing the variant resulting from steps b-d,

g) testing the activity of the variant on the selected ester bond,

h) selecting a variant having an altered activity on the selected ester bond, and

i) producing the selected variant.

2. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme having a structure comprising a catalytic triad consisting of an active Ser, an active Asp and an active His residue,

c) in the parent lipolytic enzyme selecting at least one amino acid residue comprising at least one atom belonging to a set E defined by the following steps:

i) aligning the structure of the lipolytic enzyme with *Rhizomucor miehei* lipase structure 4TGL comprising a catalytic triad and an inhibitor phosphorus atom (4TGL-inhP), so as to minimize the sum of squares

of deviation between atoms of the catalytic triads of the two structures,

ii) defining a set A consisting of atoms of the lipolytic enzyme inside a sphere of radius 18 Å with center at 4TGL-inhP,

iii) forming a first plane defined by 4TGL-inhP, the Cα atom of the active Ser residue of the parent lipolytic enzyme, and the Cα atom of the active Asp residue of the parent lipolytic enzyme and defining a set B as a subset of set A consisting of atoms on the same side of the first plane as the Cα atom of the active His residue of the parent lipolytic enzyme,

iv) forming a second plane defined by 4TGL-inhP, the Cα atom of the active Ser residue of the parent lipolytic enzyme, and the Cα atom of the active His residue of the parent lipolytic enzyme and defining a set C as a subset of set A consisting of atoms on the opposite side of the second plane from the Cα atom of the active Asp residue of the parent lipolytic enzyme,

v) forming a set D consisting of atoms belonging to the union of sets B and C, and having a solvent accessibility of 15 or higher, and

vi) forming set E consisting of amino acid residues in the structure which comprise an atom belonging to set D or an atom belonging to the union of sets B and C and located less than 3.5 Å from an atom belonging to set D,

d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than d),

f) preparing the variant resulting from steps d) - f), and

g) testing the activity of the variant on the selected ester bond,

h) selecting a variant having an altered activity on the selected ester bond, and

i) producing the selected variant.

3. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme having an active site comprising an active His residue,

c) in the amino acid sequence of the parent lipolytic enzyme selecting at least one amino acid residue at the C-terminal side of the active His residue,

d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

f) preparing the variant resulting from steps b-d,

g) testing the activity of the variant on the selected ester bond,

h) selecting a variant having an altered activity on the selected ester bond, and

i) producing the selected variant.

4. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme,

c) selecting at least one amino acid residue among 10 amino acid residues at the C-terminal,

d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),

f) preparing the variant resulting from steps c) - e),

g) testing the activity of the variant on the selected ester bond,

h) selecting a variant having an altered activity on the selected ester bond, and

i) producing the selected variant.

5. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme having a lid,

c) selecting at least one amino acid residue in the lid,

d) making alterations each of which is an insertion, a deletion or a substitution of the selected amino acid residues,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),

f) preparing the variant resulting from steps c) - e),

g) testing the activity of the variant on the selected ester bond,

h) selecting a variant having an altered activity on the selected ester bond, and

i) producing the selected variant.

6. The method of any of claims 1-5 wherein the lipolytic enzyme is native to an eukaryote, preferably to a fungus, and most preferably belongs to the *Humicola* family or the *Zygomycetes* family.

7. A method of producing a lipolytic enzyme variant comprising:

a) selecting a substrate and an ester bond of interest,

b) selecting a parent lipolytic enzyme from the *Humicola* family or the *Zygomycetes* family,

c) selecting at least one amino acid residue corresponding to any of amino acids 20-25, 56-64, 81-85 and 255-269 in the *Humicola lanuginosa* lipase

d) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

e) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),

f) preparing the variant resulting from steps b-e,

g) testing the activity of the variant on the ester bond in the substrate, and

h) selecting a variant having an altered activity on the ester bond.

8. The method of claim 7 wherein the parent lipolytic enzyme is the lipase of *Humicola lanuginosa* strain DSM 4109.

9. The method of any of claims 1-8 wherein the altered activity is a lower activity towards a C_4-C_8 acyl bond in a triglyceride, or a lower ratio of activity towards a C_4-C_8 acyl bond in a triglyceride and a C_{16}-C_{20} acyl bond in a triglyceride.

10. The method of claim 9 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.

11. The method of any of claims 1-8 wherein the altered activity is a lower activity towards a C_{16}-C_{20} acyl bond in a triglyceride, or a lower ratio of activity towards a C_{16}-C_{20} acyl bond in a triglyceride and a C_4-C_8 acyl bond in a triglyceride.

12. The method of any of claims 1-8 wherein the altered activity is a higher phospholipase activity.

13. The method of claim 12 wherein the parent lipolytic enzyme has a phospholipase activity below 50 PHLU/mg and/or a ratio of phospholipase activity to lipase activity below 0,1 PHLU/LU.

14. The method of claim 12 or 13 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to R81, R84, S85, or 263-267 (e.g. G266 or T267) in the *Humicola lanuginosa* lipase.

15. The method of any of claims 12-14 wherein the alterations comprise insertion of a peptide extension at the C-terminal, preferably comprising 1-5 amino acid residues, the first preferably being A, P or D, the second (if present) preferably being V, G or

R, the third (if present) preferably being V, G or R, the fourth (if present) preferably being F, and the fifth (if present) preferably being S.

16. The method of any of claims 1-8 wherein the altered activity is a higher hydrolytic activity on a digalactosyl-diglyceride.

17. The method of claim 16 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109, and the selected amino acid residues comprise an amino acid corresponding to 21, 23, 26, 57, 62, 81, 83, 84, 85, 266, 267 or 269 in the *Humicola lanuginosa* lipase.

18. A method of preparing a lipolytic enzyme variant for use in baking, which method comprises:

a) selecting a parent lipolytic enzyme,

b) making at least one alteration which is an insertion, a deletion or a substitution of an amino acid residue in the lipolytic enzyme to obtain a lipolytic enzyme variant,

c) screening for a lipolytic enzyme variant which compared to the parent lipolytic enzyme has:

i) a higher ratio selectivity for long-chain fatty acyl groups,

ii) a higher activity on digalactosyl diglyceride, and

iii) a higher phospholipase activity, and

d) preparing the lipolytic enzyme variant.

19. The method of claim 18 wherein the parent lipolytic enzyme and the amino acid to be altered are selected as defined in any of claims 1-8.

20. A method of preparing a lipolytic enzyme variant for use in baking, which method comprises

a) subjecting a DNA sequence encoding a lipolytic enzyme to random mutagenesis,

b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and

c) screening for host cells expressing a lipolytic enzyme variant which compared to the parent lipolytic enzyme has:

i) a higher ratio selectivity for long-chain fatty acyl groups,

ii) a higher activity on digalactosyl diglyceride, and

iii) a higher phospholipase activity, and

d) preparing the lipolytic enzyme expressed by the host cells.

21. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having an alcohol binding site having a glycerol part with an sn2 position, which variant:

a) comprises an alteration which is an insertion, a deletion or a substitution of an amino acid residue, at a position which in a three-dimensional structure of the parent lipolytic enzyme and a substrate is within 10 Å of the C atom at the sn2 position of the glycerol part of a substrate triglyceride, and

b) has an altered activity on an ester bond in the substrate.

22. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having a lid, which variant:

a) comprises an alteration which is an insertion, a deletion or a substitution of an amino acid residue in the lid,

b) has an altered activity on an ester bond in the substrate.

23. A lipolytic enzyme which is a variant of a parent lipolytic enzyme having an active site comprising an active His residue, which variant:

a) comprises an alteration which is an insertion, a deletion or a substitution of at least one amino acid residue at the C-terminal side of the active His residue,

b) has an altered activity on an ester bond in a substrate.

24. A lipolytic enzyme which is a variant of a parent lipolytic enzyme, which variant:

a) comprises an alteration which is an insertion, a deletion or a substitution of at least one amino acid within 10 amino acid residues of the C-terminal,

b) has an altered activity on an ester bond in a substrate.

25. The lipolytic enzyme of any of claims 21-24 wherein the parent lipolytic enzyme is native to an eukaryote, preferably to a fungus, and most preferably belongs to the *Zygomycetes* family.

26. The lipolytic enzyme of claim 25 wherein the parent lipolytic enzyme belongs to the *Humicola* family or the *Zygomycetes* family, preferably the lipase of *Humicola lanuginosa* strain DSM 4109.

27. A lipolytic enzyme which:

a) is a polypeptide having an amino acid sequence which has at least 80 % homology with a reference lipolytic enzyme of the *Humicola* family or the *Zygomycetes* family;

b) compared to said reference lipolytic enzyme comprises an amino acid alteration which is:

i) a substitution, deletion or insertion at a position corresponding to A20, Y21, G23, K24, N25, V63, R81, G82, R84, A257, W260, Y261, F262 or G266 in the *Humicola lanuginosa* DSM 4109 lipase;

ii) a substitution of an amino acid corresponding to C268 or L269 in said lipase;

iii) a substitution corresponding to V60G, D62E, L93K, L97Q, K98E,F, E99D, P256A, G263E,Q,R,F,N, L264A,C,P,F,G,V,I, I265L,N,F or T267A,Q,P,S,V,E in said lipase;

iv) an insertion corresponding to T267GS or T267GL in said lipase;

v) a peptide extension at the C-terminal which is A, P, MD, CP, AG, DG, AGG, PVGF, AGRF, PRGF, AGGF or AGGFS;

vi) a peptide extension at the C-terminal of 40-50 amino acids; or

vii) a truncation of 1, 2, 3, 4, 5 or 6 amino acids at the C-terminal; and

c) has an altered activity on an ester bond in a substrate compared with the reference lipolytic enzyme.

28. The lipolytic enzyme of claim 27 wherein the amino acid alteration corresponds to R84K,L,W, W260H,Q,C, G266A,C,D,N,L,I,S,T,P,V,F,W,E,K,R,Y or L269N,I,S.

29. The lipolytic enzyme of claim 27 or 28 which further comprises at least one further amino acid alteration which is a substitution, a deletion or an insertion corresponding to any of positions 22, 56-59, 61, 64, 83, 85, 91, 94, 249, 255 or 259 preferably S83T, G91A, N94D, D96S,W,F,G, Q249R or L259N,R,S,M,Q.

30. The lipolytic enzyme of any of claims 27-29 which further comprises a substitution corresponding to D62A,G,V, K98D, E99K, P256T, G263A and/or I265T,G,V.

31. The lipolytic enzyme of any of claims 27-30 which comprises a peptide extension at the N-terminal.

32. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Humicola lanuginosa*.

33. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Rhizomucor miehei*.

34. The lipolytic enzyme of any of claims 27-31 wherein the reference lipolytic enzyme is the lipase from *Fusarium oxysporum*.

35. A lipolytic enzyme which:

a) is a polypeptide having an amino acid sequence which has at least 80 % homology with a reference enzyme which is the lysophospholipase from *Aspergillus foetidus*, the ferulic acid esterase from *Aspergillus niger*, the ferulic

acid esterase from *Aspergillus tubigensis* or phospholipase A1 from *Aspergillus oryzae*,

b) compared to said reference enzyme comprises an amino acid alteration which is a substitution, deletion or insertion at a position corresponding to 20-25, 56-64, 81-85, 91-98, 255-257 or 259-269 in the *Humicola lanuginosa* lipase, and

c) has an altered activity on an ester bond in a substrate compared with the reference enzyme.

36. The lipolytic enzyme of claim 35 wherein the alteration is at a position corresponding to Y21, E56, D57, V60, G61, D62, S83, R84, G91, L93, N94, D96, L97, K98, E99, P256, W260, Y261, G263, L264, I265, G266, T267 or L269 in the *Humicola lanuginosa* lipase

37. The lipolytic enzyme of claim 35 or 36 wherein the alteration is an extension or a truncation at the C-terminal, preferably by 1-5 amino acids.

38. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a lower activity towards a C_4-C_8 acyl bond in a triglyceride, or a lower ratio of activity towards a C_4-C_8 acyl bond in a triglyceride and a C_{16}-C_{20} acyl bond in a triglyceride.

39. The lipolytic enzyme of claim 38 which comprises an amino acid alteration at a position corresponding to Y21, E56, D57, V60, G61, D62, R81, S83, R84, L259, Y261 or G266 in the *Humicola lanuginosa* lipase.

40. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a lower activity towards a C_{16}-C_{20} acyl bond in a triglyceride, or a lower ratio of activity towards a C_{16}-C_{20} acyl bond in a triglyceride and a C_4-C_8 acyl bond in a triglyceride.

41. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a higher phospholipase activity.

42. The lipolytic enzyme of claim 41 which comprises an amino acid alteration at a position corresponding to R81, R84, S85, G263, L264, I265, G266, T267 or L269 in the *Humicola lanuginosa* lipase, preferably a substitution corresponding to G263A,E,Q,R; L264A,C,P,Q; I265L,N,T; G266A, C, D, N, L, I, S, T, P, V or T267A,Q or L269N.

43. The lipolytic enzyme of claims 41 or 42 which has a phospholipase activity greater than 0.1 nmol/min in a monolayer assay at pH 5 as described herein and/or a phospholipase activity greater than 100 PHLU/mg (preferably greater than 500 PHLU/mg) and/or a ratio of phospholipase activity to lipase activity greater than 0.1 PHLU/LU (preferably greater than 0.5 PHLU/LU).

44. The lipolytic enzyme of any of claims 41-43 wherein the parent lipolytic enzyme has a phospholipase activity below 50 PHLU/mg and/or a ratio of phospholipase activity to lipase activity below 0,1 PHLU/LU.

45. The lipolytic enzyme of any of claims 41-44 which comprises a peptide extension at the C-terminal, preferably comprising 1-5 amino acid residues, the first preferably being A, P or D, the second (if present) preferably being V, G or R, the third (if present) preferably being V, G or R, the fourth (if present) preferably being F, and the fifth (if present) preferably being S.

46. The lipolytic enzyme of any of claims 41-45 which comprises a deletion of amino acid residues at positions corresponding to positions C268 and L269 in the lipase of *Humicola lanuginosa* strain DSM 4109.

47. The lipolytic enzyme of any of claims 27-37 wherein the altered activity is a higher hydrolytic activity on a digalactosyl-diglyceride.

48. The lipolytic enzyme of claim 47 which comprises an amino acid alteration at a position corresponding to Y21, G23, N26, D57, D62, R81, S83, R84, S85, G266, T267 or L269 in the *Humicola lanuginosa* lipase, preferably comprising two or more

such alterations, most preferably further comprising at least one alteration in the lid region

49. The lipolytic enzyme of any of claims 27-48 which comprises an alteration in the lid which is a substitution of a negatively charged amino acid residue with a neutral or positively charged amino acid residue, or a substitution of a neutral amino acid residue with a positively charged amino residue.

50. The lipolytic enzyme of claim 49 which comprises an alteration in the lid at a position corresponding to position G91, D96 and/or E99 in the *Humicola lanuginosa* lipase, preferably a substitution which is G91A, D96S,W,F or E99K.

51. A lipolytic enzyme which is a variant of a parent lipase derived from *Humicola lanuginosa* strain DSM 4109 comprising the alterations E1E,D,A+ G91G,A,S,T+ N94N,D+ D96D,G,F,W+ E99E,K+ G225G,R,K+ G263Q,N+ L264L,A,V+ I265I,T,S+ G266G,A,V,S,D,E+ T267T,A,V+ L269L,I,N,Q.

52. The lipolytic enzyme of claim 51 which further comprises SPIRR as a peptide extension at the N-terminal and/or AGGF or AGGFS as a peptide extension at the C-terminal.

53. A DNA sequence encoding the lipolytic enzyme of any of claims 27-52.

54. A vector comprising the DNA sequence of claim 53.

55. A transformed host cell harboring the DNA sequence of claim 53 or the vector of claim 54.

56. A method of producing the lipolytic enzyme of any of claims 27-52 comprising

a) cultivating the cell of claim 55 so as to express and preferably secrete the lipolytic enzyme, and

b) recovering the lipolytic enzyme.

57. A process for preparing a dough or a baked product prepared from the dough which comprises adding the lipolytic enzyme of any of claims 27-52 to the dough, wherein the lipolytic enzyme preferably has phospholipase and/or digalactosyl diglyceride activity.

58. The process of claim 57 which further comprises adding to the dough an endo-amylase and/or a phospholipid.

59. The process of claim 57 or 58 wherein the endo-amylase is from *Bacillus*, and is preferably a maltogenic amylase from *B. stearothermophilus*,

60. A process for reducing the content of phospholipid in an edible oil, comprising treating the oil with the lipolytic enzyme of any of claims 41-46, 51 or 52 so as to hydrolyze a major part of the phospholipid, and separating an aqueous phase containing the hydrolyzed phospholipid from the oil.

61. A process for improving the filterability of an aqueous solution or slurry of carbohydrate origin which contains phospholipid, which process comprises treating the solution or slurry with the lipolytic enzyme of any of claims 41-46, 51 or 52, wherein the solution or slurry preferably contains a starch hydrolysate, particularly a wheat starch hydrolysate.

62. A detergent composition comprising a surfactant and the lipolytic enzyme of any of claims 27-52, wherein the lipolytic enzyme preferably has a specificity for long-chain fatty acids corresponding to a ratio of SLU to LU above 3.

63. A method of enhancing the flavor of a food product containing milk fat, comprising treating the food product with the lipolytic enzyme of any of claims 27-52 so as to release free fatty acids, wherein the lipolytic enzyme preferably has a specificity for short-chain fatty acids corresponding to a ratio of SLU to LU below 0.5, more preferably below 0.2, e.g. below 0.1.

64. A method of preparing a dough or a baked product prepared from the dough, comprising:

a) testing at least one lipolytic enzyme for its hydrolytic activity towards a C_4-C_8 acyl bond in a triglyceride, a C_{16}-C_{20} acyl bond in a triglyceride, digalactosyl diglyceride and a phospholipid,

b) selecting a lipolytic enzyme having hydrolytic activity towards digalactosyl diglyceride and the phospholipid, and having a ratio of activity towards the C_{16}-C_{20} acyl bond and the C_4-C_8 acyl bond which corresponds to a SLU/LU ratio of at least 3, and

c) adding the selected lipolytic enzyme to the dough.

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(57) Abstract

The substrate specificity of a lipolytic enzyme can be modified by making alterations to the amino acid sequence in a defined region of the lipolytic enzyme, so as to increase the level of a desired activity or to decrease the level of an undesired activity. Thus, the inventors have developed lipolytic enzyme variants with a modified amino acid sequence with a substrate specificity which can be tailored for specific uses.

```
          1                                                  50
rhimi     SIDGGIRAAT SQEINELTYY TTLSANSYCR TVIPGA...T WDC..IHCDA
rhidl     SDGGKVVAAT TAQIQEFTKY AGIAATAYCR SVVPGN...K WDC..VQCQK
SP400     --------EVS QDLFNQFNLF AQYSAAAYCG KNNDAPAGTN ITCTGNACPE
  Pcl     --------DVS TSELDQFEFW VQYAAASYYE ADYTAQVGDK LSCSKGNCPE
FoLnp11   -----AVGVT TTDFSNFKFY IQHGAAAYC. .NSEAAAGSK ITCSNNGCPT

          51                                                 100
rhimi     TE..DLKIIK TWS.TLIYDT NAMVARGDSE KTIYIVFRGS SSIRNWIADL
rhidl     WV.PDGKIIT TFT.SLLSDT NGYVLRSDKQ KTIYLVFRGT NSFRSAITDI
SP400     VEKADATFLY SFEDSGVGDV TGFLALDNTN KLIVLSFRGS RSIENWIGNL
  Pcl     VEATGATVSY DFSDSTITDT AGYIAVDHTN SAVVLAFRGS YSVRNWVADA
FoLnp11   VQGNGATIVT SFVG.SKTGI GGYVATDSAR KEIVVSFRGS INIRNWLTNL

          101                                                150
rhimi     TFVPVSY.PP VSGTKVHKGF LDSYGEVQNE LVATVLDQFK QYPSYKVAVT
rhidl     VFNFSDY.KP VKGAKVHAGF LSSYEQVVND YFPVVQEQLT AHPTYKVIVT
SP400     NFDLKEINDI CSGCRGHDGF TSSWRSVADT LRQKVEDAVR EHPDYRVVFT
  Pcl     TFVHTNP.GL CDGCLAELGF WSSWKLVRDD IIKELKEVVA QNPNYELVVV
FoLnp11   DFGQEDC.SL VSGCGVHSGF QRAWNEISSQ ATAAVASARK ANPSFNVIST

          151                                                200
rhimi     GHSLGGATAL LCALDLYQRE EGLSSSNLFL YTQGQPRVGD PAFANYVVST
rhidl     GHSLGGAQAL LAGMDLYQRE PRLSPKNLSI FTVGGPRVGN PTFAYYVEST
SP400     GHSLGGALAT VAGADLRGN. .GY...DIDV FSYGAPRVGN RAFAEFLTVQ
  Pcl     GHSLGAAVAT LAATDLRGK. .GYP..SAKL YAYASPRVGN AALAKYITAQ
FoLnp11   GHSLGGAVAV LAAANLRVG. .GT...PVDI YTYGSPRVGN AQLSAFVSNQ

          201                                                250
rhimi     G.IPYRRTVN ERDIVPHLPP AAFGFLHAGE EYWITD.NSP ......ETVQ
rhidl     G.IPFQRTVH KRDIVPHVPP QSFGFLHPGV ESWIKS.GT. ......SNVQ
SP400     TGGTLYRITH TNDIVPRLPP REFGYSHSSP EYWIKS.GTL V.PVTRNDIV
  Pcl     G..NNFRFTH TNDPVPKLPL LSMGYVHVSP EYWITS.PNN A.TVSTSDIK
FoLnp11   A.GGEYRVTH ADDPVPRLPP LIFGYRHTTP EFWLSGGGGD KVDYTISDVK

          251                                                300
rhimi     VCTSDLETSD CSNSIVPFT. .SVLDHLSYF GINTGLCT-- ----------
rhidl     ICTSEIETKD CSNSIVPFT. .SILDHLSYF DINEGSCL-- ----------
SP400     KIEGID.ATG GNNQP.NIP. .DIPAHLWYF .GLIGTCL-- ----------
  Pcl     VIDGDV.SFD GNTGTGLPLL TDFEAHIWYF .VQVDAGKGP GLPFKRV---
FoLnp11   VCEGAA.NLG CNGGT.LGL. .DIAAHLHYF .QATDACNAG GFSWRRYRSA

          301                                              338
rhimi     ---------- ---------- ---------- -----...
rhidl     ---------- ---------- ---------- -----...
SP400     ---------- ---------- ---------- -----...
  Pcl     ---------- ---------- ---------- -----...
FoLnp11   ESVDKRATMT DAELEKKLNS YVQMDKEYVK NNQARS..
```

Fig. 1

Alignment of lipase sequences

Attorney Docket No.: 5559.204-US PATENT

COMBINED DECLARATION FOR UTILITY PATENT APPLICATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, mailing address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

LIPOLYTIC ENZYME VARIANTS
(Title of the Invention)

the specification of which
[ ] is attached hereto
OR
[x] was filed on 11/29/1999, as PCT International Application Number **PCT/DK99/00664** and was amended on (MM/DD/YYYY) _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by an amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56, including for continuation-in-part applications, material information which became available between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT international applications(s) for patent or inventor's certificate or of any PCT international applications(s) which designated at least one country other than the United States of America, listed below and have also identified below any foreign application(s) for patent or inventor's certificate, or any PCT international application(s) having a filing date before that of the application(s) on which priority is claimed:

Prior Foreign Application Number(s)	Country	Foreign Filing Date (MM/DD/YYYY)	Priority Claimed
PA 1998 01572	Denmark	11/27/1998	[x] YES [ ] NO
PA 1999 00391	Denmark	03/22/1999	[x] YES [ ] NO
PA 1999 01481	Denmark	10/15/1999	[x] YES [ ] NO
			[ ] YES [ ] NO

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States provisional application(s) listed below.

Application Number(s)	Filing Date
60/111,430	12/08/1998
60/126,914	03/29/1999
60/160,735	10/22/1999

Direct all correspondence to:

Customer Number **25908**

I hereby appoint the practitioners at the above mentioned customer number as my/our attorney(s) or agent (s) to prosecute the application identified above, and to transact all business in the United States Patent and Trademark Office connected therewith.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00

NAME OF SOLE OR FIRST INVENTOR	
Given Name (first and middle [if any])	Kirsten
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NAME OF SECOND INVENTOR	
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Given Name (first and middle [if any])	Claus Crone
Family Name or Surname	Fuglsang
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Citizenship	Danish
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NAME OF FOURTH INVENTOR	
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Citizenship	Danish
Mailing Address	Christoffers Allé 91
City, State, Zip, Country	DK-2800 Lyngby, Denmark

NAME OF FIFTH INVENTOR	
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Family Name or Surname	Borch
Inventor's Signature	
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Residence: City, State, Country	Birkerød, Denmark
Citizenship	Danish
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City, State, Zip, Country	DK-3460 Birkerød, Denmark

NAME OF SIXTH INVENTOR	
Given Name (first and middle [if any])	Jesper
Family Name or Surname	Vind
Inventor's Signature	
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Citizenship	Danish
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City, State, Zip, Country	DK-2800 Lyngby, Denmark

NAME OF SEVENTH INVENTOR	
Given Name (first and middle [if any])	Andreas
Family Name or Surname	Petri
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Date	
Residence: City, State, Country	Copenhagen, Denmark
Citizenship	Danish
Mailing Address	Tagensvej
City, State, Zip, Country	DK-2200 Copenhagen, Denmark

NAME OF EIGHTH INVENTOR	
Given Name (first and middle [if any])	Sanne O. Schrøder
Family Name or Surname	Glad
Inventor's Signature	
Date	
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Citizenship	Danish
Mailing Address	Viggo Barfoeds Allé 59
City, State, Zip, Country	DK-2750 Ballerup, Denmark

NAME OF NINTH INVENTOR	
Given Name (first and middle [if any])	Gitte
Family Name or Surname	Budolfsen
Inventor's Signature	
Date	
Residence: City, State, Country	Frederiksberg, Denmark
Citizenship	Danish
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City, State, Zip, Country	DK-2000 Frederiksberg, Denmark

Attorney Docket No.: 5559.204-US PATENT

COMBINED DECLARATION FOR UTILITY PATENT APPLICATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, mailing address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

LIPOLYTIC ENZYME VARIANTS

(Title of the Invention)

the specification of which
[ ] is attached hereto
OR
[x] was filed on 11/29/1999, as PCT International Application Number **PCT/DK99/00664** and was amended on (MM/DD/YYYY) _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by an amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56, including for continuation-in-part applications, material information which became available between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

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PA 1999 01481	Denmark	10/15/1999	[x] YES [ ] NO
			[ ] YES [ ] NO

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States provisional application(s) listed below.

Application Number(s)	Filing Date
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Direct all correspondence to:

Customer Number **25908**

I hereby appoint the practitioners at the above mentioned customer number as my/our attorney(s) or agent (s) to prosecute the application identified above, and to transact all business in the United States Patent and Trademark Office connected therewith.

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NAME OF SOLE OR FIRST INVENTOR	
Given Name (first and middle [if any])	Kirsten
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Citizenship	Danish
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City, State, Zip, Country	DK-2900 Hellerup, Denmark

2-00

NAME OF SECOND INVENTOR	
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Citizenship	Danish
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3-00

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Citizenship	Danish
Mailing Address	Poppelhøj 43
City, State, Zip, Country	DK-2990 Nivå, Denmark

4-00

NAME OF FOURTH INVENTOR	
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Citizenship	Danish
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5-00

NAME OF FIFTH INVENTOR	
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Family Name or Surname	Borch
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Citizenship	Danish
Mailing Address	Vandtårnsvej 18
City, State, Zip, Country	DK-3460 Birkerød, Denmark

6-00

NAME OF SIXTH INVENTOR	
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Family Name or Surname	Vind
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Citizenship	Danish
Mailing Address	Bagsværdvej 115
City, State, Zip, Country	DK-2800 Lyngby, Denmark

7-00

NAME OF SEVENTH INVENTOR	
Given Name (first and middle [if any])	Andreas
Family Name or Surname	Petri
Inventor's Signature	
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Citizenship	Danish
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City, State, Zip, Country	DK-2200 Copenhagen, Denmark

8-00

NAME OF EIGHTH INVENTOR	
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Family Name or Surname	Glad
Inventor's Signature	
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Citizenship	Danish
Mailing Address	Viggo Barfoeds Allé 59
City, State, Zip, Country	DK-2750 Ballerup, Denmark

9-00

NAME OF NINTH INVENTOR	
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Family Name or Surname	Budolfsen
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Citizenship	Danish
Mailing Address	Lyøvej 3, 3.tv.
City, State, Zip, Country	DK-2000 Frederiksberg, Denmark

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